

STIC-Biotech/ChemLib

74854

From: Spector, Lorraine
Sent: Wednesday, September 04, 2002 9:35 AM
To: STIC-Biotech/ChemLib
Subject: Serial No. 09/912436

Please search SEQ ID NO:5 and 6

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

-pending
-issued
-commercial

I am interested in hits that are slightly LESS than 100% identical- please print results down to 90% identity, at least.

Also particularly interested in mutations at nucleotides 286-294 of SEQ ID NO:5, if there's any way to search for that specifically.

Thanks.

Lorraine Spector
703-308-1793
U.S. Patent and Trademark Office
Art Unit 1646
lorraine.spector@uspto.gov
CM1-10B11

10D19
~~10B11~~

RECEIVED
SEP - 4 2002
STIC

Searcher: M. Smith
Phone: _____
Location: _____
Date Picked Up: 9/5/02
Date Completed: 9/10/02
Searcher Prep/Review: 10
Clerical: 4
Online time: 10

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 01:51:17 : Search time 24.91 Seconds

(Without alignments)
133.355 Million cell updates/sec

Title: US-09-912-436-6

Sequence: 1 MSPLRLRLALQLAPAQ.....EEHSCCECRPKKDSAVKPD 136

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

231622

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 99%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	89.6	188	1	US-08-469-427A-5
2	644	89.6	188	2	US-08-609-443B-5
3	644	89.6	188	2	US-08-569-063C-5
4	641	89.2	207	2	US-08-609-443B-13
5	641	89.2	207	2	US-08-569-063C-13
6	630.5	87.7	195	1	US-08-469-427A-7
7	630.5	87.7	195	2	US-08-609-443B-7
8	630.5	87.7	195	2	US-08-569-063C-7
9	612	85.1	133	1	US-08-469-427A-9
10	612	85.1	133	2	US-08-609-443B-9
11	612	85.1	133	2	US-08-569-063C-9
12	489	68.0	102	1	US-08-469-427A-2
13	489	68.0	102	2	US-08-609-443B-2
14	489	68.0	102	2	US-08-569-063C-2
15	269.5	37.5	146	4	US-08-586-039B-33
16	269.5	37.5	146	4	US-08-586-039B-31
17	269.5	37.5	146	4	US-08-586-039B-35
18	266.5	37.1	190	6	5332671-3
19	264.5	36.8	190	2	US-08-369-063C-20
20	264.5	36.8	190	2	PCT-US96-09001-10
21	264	36.7	147	4	US-08-807-992B-1
22	264	36.7	147	4	US-09-392-932-1
23	264	36.7	191	3	US-08-567-200A-2
24	264	36.7	191	3	US-08-807-992B-2
25	264	36.7	191	3	US-08-691-794-2
26	264	36.7	191	4	US-08-795-430-56
27	264	36.7	191	4	US-09-392-932-3

28	264	36.7	191	6	5332671-4	Patent No. 5332671
29	264	36.7	214	6	5240848-11	Patent No. 5240848
30	264	36.7	215	3	US-08-807-992B-3	Sequence 3, Appl
31	264	36.7	215	6	US-08-586-039B-49	Sequence 49, Appl
32	264	36.7	215	6	5240848-7	Patent No. 5240848
33	264	36.7	232	2	US-08-999-811-7	Sequence 7, Appl
34	264	36.7	232	2	US-08-824-996-9	Sequence 9, Appl
35	264	36.7	232	2	US-08-807-992B-4	Sequence 4, Appl
36	264	36.7	232	3	US-09-042-105-7	Sequence 7, Appl
37	263	36.6	215	6	5219739-22	Patent No. 5219739
38	257	35.7	109	3	US-08-691-794-3	Sequence 3, Appl
39	257	35.7	110	4	US-09-392-932-11	Sequence 11, Appl
40	257	35.7	121	6	5194596-19	Patent No. 5194596
41	257	35.7	121	6	5219739-20	Patent No. 5219739
42	257	35.7	145	3	US-08-784-551C-2	Sequence 2, Appl
43	257	35.7	145	4	US-09-392-932-2	Sequence 2, Appl
44	257	35.7	165	6	5194596-18	Patent No. 5194596
45	257	35.7	165	6	5219739-19	Patent No. 5219739

ALIGNMENTS

RESULT 1
US-08-469-427A-5
Sequence 5, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alfalo, Kari
APPLICANT: Patuola, Kari
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF INVENTIONS: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8844
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-5

[illegible]

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RESULT 2
US-08-609-443B-5
Sequence 5, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-609-443B-5

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1      RESULT      3
2      US-08-569-063C-5
3      Sequence 5, Application US/08569063C
4      Patent No. 5928939
5      GENERAL INFORMATION:
6      APPLICANT: ERIKSSON, ULF
7      APPLICANT: OLOFSSON, Birgitta
8      APPLICANT: ALITALO, Kari
9      APPLICANT: PAUISOLA, Kari
10     TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
11     TITLE OF INVENTION: DNA CODING THEREFOR
12     NUMBER OF SEQUENCES: 23
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
15     STREET: 1200 G Street, N.W., Suite 700
16     CITY: Washington
17     STATE: DC
18     COUNTRY: USA
19     ZIP: 20005
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patentin Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/569,063C
27     FILING DATE: 06-DEC-1995
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 08/469,427
30     FILING DATE: 06-JUN-1995
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: US 08/397,651
33     FILING DATE: 01-MAR-1995
34     ATTORNEY/AGENT INFORMATION:
35     NAME: EVANS, Joseph D
36     REGISTRATION NUMBER: 26,269
37     REFERENCE/DOCKET NUMBER: 1064/41979CP3
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: (202) 628-8800
40     TELEFAX: (202) 628-8844
41     INFORMATION FOR SEQ ID NO: 5:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 188 amino acids
44     TYPE: amino acid
45     STRANDEDNESS: single
46     TOPOLOGY: linear
47     MOLECULE TYPE: protein
48     HYPOTHETICAL: NO
49     ORIGINAL SOURCE:
50     TISSUE TYPE: adult mouse heart
51     ?
52     ?
53     US-08-569-063C-5
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56 Best Local Similarity      89.08;      Pred. No. 1,3e-66;

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Oy	121	QCECRPRKKDSAVKPD	136
Dd	121	QCECRPRKKESAVKPD	136

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        1 .....:.....:.....:.....:.....:.....:.....:.....:.....:
Db      61 MGNVYKOLVPSCVYTORCGGCCPPDGEVCYPTGQHGYRMQYPRGPMGQILMIQYRPSQLGE 120
Oy      114 MSLEHSQCECRPPKKDSAVVPD 136
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DB 121 MSLEHSQCCECRPKKESAVRD 143

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Best Local Similarity	84.6%;	Pred. No. 6e-67;		
Matches 121; Conservative	5;	Mismatches	10;	Gaps 1;

[illegible]

Db 121 MSLEHSSOCECRPKKESAVKPD 143

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|||||
RESULT 8
US-08-569-063C-7
; Sequence 7, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-7
```

```
Query Match 87.7%; Score 630.5; DB 2; Length 195;
Best Local Similarity 84.6%; Pred. No. 6e-67;
Matches 121; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

Qy 1 MSPILRLLLAALLQAPAVSOPDAPGHQKRVSWIDVYTRATCQPREVVVPLTVEL 60
Db 1 MSPILRLLLAALLQAPAVSOPDAPGHQKRVSWIDVYTRATCQPREVVVPLSMEL 60

Qy 61 MGTAKQLVPSCVTVQRCGCCPDGDLCEVPTGQHVRM-----QILMIRYPSQGLGE 113
Db 61 MGNVVKQLVPSCVTVQRCGCCPDGDLCEVPTGQHVRMQLMIRYPSQGLGE 120

Qy 114 MSLEHSSOCECRPKKESAVKPD 136
Db 121 MSLEHSSOCECRPKKESAVKPD 143
```

```
RESULT 9
US-08-469-427A-9
; Sequence 9, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-427A-9
```

```
Query Match 85.1%; Score 612; DB 1; Length 133;
Best Local Similarity 89.1%; Pred. No. 5.7e-65;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MSPILRLLLAALLQAPAVSOPDAPGHQKRVSWIDVYTRATCQPREVVVPLTVEL 60
Db 1 MSPILRLLLAALLQAPAVSOPDAPGHQKRVSWIDVYTRATCQPREVVVPLSMEL 60

Qy 61 MGTAKQLVPSCVTVQRCGCCPDGDLCEVPTGQHVRMQLMIRYPSQGLGEKSLSEHS 120
Db 61 MGNVVKQLVPSCVTVQRCGCCPDGDLCEVPTGQHVRMQLMIRYPSQGLGEKSLSEHS 120

Qy 121 OCECRPKK 129
Db 121 OCECRPKK 129

RESULT 10
US-08-609-443B-9
; Sequence 9, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
```

APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-443B-9

Query Match 85.1%; Score 612; DB 2; Length 133;
Best Local Similarity 89.1%; Pred. No. 5.7e-65;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 MSPFLRRLILALDLQAPAPVSPDAPGHORRVSMIDVYTRATCPREVVPLTVEL 60
DB 1 MSPFLRRLILVALLQARQAPVSPDGFPSHOKKVPWIDVYARATCPREVVPLSMEL 60
QY 61 MGTVAQVLVPCVTVQRCGCCPDGDLCEVPTGQHOVRMQLIMIRYSSQLGEMSLSEHS 120
DB 61 MGTVAQVLVPCVTVQRCGCCPDGDLCEVPTGQHOVRMQLIMIRYSSQLGEMSLSEHS 120
QY 121 OCECRPKK 129
DB 121 OCECRPKK 129

RESULT 11
US-08-565-063C-9
Sequence 9, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Katri
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-063C-9

Query Match 85.1%; Score 612; DB 2; Length 133;
Best Local Similarity 89.1%; Pred. No. 5.7e-65;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 MSPFLRRLILALDLQAPAPVSPDAPGHORRVSMIDVYTRATCPREVVPLTVEL 60
DB 1 MSPFLRRLILVALLQARQAPVSPDGFPSHOKKVPWIDVYARATCPREVVPLSMEL 60
QY 61 MGTVAQVLVPCVTVQRCGCCPDGDLCEVPTGQHOVRMQLIMIRYSSQLGEMSLSEHS 120
DB 61 MGTVAQVLVPCVTVQRCGCCPDGDLCEVPTGQHOVRMQLIMIRYSSQLGEMSLSEHS 120
QY 121 OCECRPKK 129
DB 121 OCECRPKK 129

RESULT 12
US-08-469-427A-2
Sequence 2, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Katri
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington

FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: mouse embryo
US-08-569-063C-2

Query Match 68.0%; Score 489; DB 2; Length 102;
Best Local Similarity 91.8%; Pred. No. 1.4e-50;
Matches 89; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 33 RKVYSWIDYTRATCPREVYVPLTELKGTVAKOLVPSCVTVQRCGCCPDGLSCVPT 92
Db 2 RPVPPIIDYARATCPREVYVPLSMELMGNYVKOLVPSCVTVQRCGCCPDGLSCVPT 61
Qy 93 GQHVRMQILMITRYPSSQLGEMSLSEHSOCECRPKK 129
Db 62 GQHVRMQILMITRYPSSQLGEMSLSEHSOCECRPKK 98

RESULT 15
US-08-586-039B-33
Sequence 33, Application US/08586039B
Patent No. 6140073
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
APPLICANT: Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,039B
FILING DATE: 16-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-586-039B-33

Query Match 37.5%; Score 269.5; DB 4; Length 146;
Best Local Similarity 43.8%; Pred. No. 2e-24;
Matches 57; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

Qy 10 LALLQLAPAAQVPSQPDARQHQR--KYVSWIDYTRATCPREVYVPLTELKGTVAQ 67
Db 12 LALLLYLHAKWSQAAPTEGEKHAHEVVKFMDVYORSYCRPLETLVDIFQETPEIEYI 71
Qy 68 LVPSCVTVQRCGCCPDGLSCVPTGQHVRMQILMITRYPSSQLGEMSLSEHSOCECRP 126
Db 72 FRPSCVPLMRKAGCCNDALSCVPTSESNTVQIMIRKPHQSHIGMSFLQHSRCRPR 131

Qy 127 KKKDSAVKPD 136
Db 132 KK--DRTKPE 139

RESULT 16
US-08-586-039B-31
Sequence 31, Application US/08586039B
Patent No. 6140073
GENERAL INFORMATION:
APPLICANT: Bayne, Marvin L.
APPLICANT: Thomas Jr., Kenneth A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
TITLE OF INVENTION: SUBUNIT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,039B
FILING DATE: 16-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/124,259
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 07/676,436
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18361DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-586-039B-31

Query Match	37.5%;	Score 269.5;	DB 4;	Length 190;
Best Local Similarity	43.8%;	Pred. NO. 2.8e-24;		
Matches 57; Conservative	21;	Mismatches 47;	Indels 5;	Gaps 3;

QY 10 LALLQLAPAOAFVSQDPABGHQR-KVYSMIDVYTRATCQPREVVPLTELMTGIVAKQ 677
 11 | | | : : | : : | : | : | : : :
 Db 12 LALLYLHNAKWSQAAPLTTEGEQKAHEVVKFMDVYGRSYCRPIETLVDFQEPDEIEYI 711

68 LVPSCVTYRGGCGCCEDDGLCEVPTGQHVRMQLIMIR-YPSOLGEMLSEHSQCERP 120
 ||| : ||| : |||| : | ||| : : : ||| : ||: |||
 Db 72 FKPSCVPLMRCAGCNDLEALCEVPTSNSVTMQIMRIKPHQSQHIGEMSLQHSRCERP 135

QY	127	KKKDSAVKPD	136
			;
Db	132	KK--DRTKPE	139

RESULT 17
US-08-586-039B-35
; Sequence 35, Application US/08586039B
; Patent No. 6140073

1 GENERAL INFORMATION:
2 APPLICANT: Bayne, Marvin L.
3 APPLICANT: Thomas, Jr., Kenneth A.
4 TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
5 TITLE OF INVENTION: SUBUNIT
6 NUMBER OF SEQUENCES: 49
7 CORRESPONDENCE ADDRESSES:

ADDRESS: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,039B
FILING DATE: 16-JAN-1996

Query Match	37.5%	Score 269.5;	DB 4;	Length 214;
Best Local Similarity	43.8%	Pred. No. 3.3e-24;		
Matches 57; Conservative	21;	Mismatches 47;	Indels 5;	Gaps 3;

```

QY 10 LALLIQLAPAPVSQDPDAPGHR--KVVSIMIDYTRATQDPREVVVLLTVELMGTVAKQ 67
    | | | | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 12 LALLYLHNKWSQAPPTTEGEKAHEVVKFMDVYQSRYSRIETLVDFIQEYDEIEYI 71

```

Qy 68 LVPSCVTVDRCGGCCDDGLBEVPTGQHVQRMQILMIR-YPPSQJGEMSELEHSHQCECRP 126
 ||||:||||:||||:||||:|:||||:||||:||||:
 Db 72 FKPSCVPLMKACGCCNDEALECVPTSEENVMTQIMRIKHKQSHGEMSFLOHRSCECRP 131

QY	127	KKKDSAVKPD	136
		:	
Db	132	KK--DRTKPE	139

RESULT 18
5332671-3
; Patent No. 5332671
; APPLICANT: FERRARA, NAPOLEONE; LEUNG, DAVID W. H.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR AND DNA ENCODING SAME

Query Match	37.1%	Score 266.5	DB 6	Length 190
Best Local Similarity	45.1%	Pred. No. 6.4e-24		
Matches 55	Conservative 22	Mismatches 42	Indels 3	Gaps 2

```

QY 10 LALLQLAPACAPVSGPDAPGHR--KUVSWIDVYTRATCQPREVVPVLTVELMGTVAKQ 67
    | | | | : : | | : : | | : | | : |
Db 12 LALLYLHNAAKWSQAPRAEGGQRPHEVVKFMDVYQSFRCRPIETLVLDVTFQEYDEIEFI 71

```

0y 68 LVPSCVTVQRGGCCDDGLCEVPTGGHVRMQLIMIR-YPSQLGEMSLSEHSOCECRP 120
 |||| : |||| : |||| : ||| : |||| : ||||
 Db 72 FKPSCVPLMKGGCCNDESLCEVPTSEENITMQLMRIKPHQSQHIGEMSLQHNKCECRP 131

QY	127	KK	128
Db	132	KK	133

RESULT 19
 US-08-569-063C-20
 : Sequence 20, Application US/08569063C
 : Patent No. 5928939
 : GENERAL INFORMATION:
 : APPLICANT: ERIKSSON, ULF
 : APPLICANT: OLOFSSON, Birgitta
 : APPLICANT: ALITALO, Kari
 : APPLICANT: PAJUSOLA, Katri
 : TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 : TITLE OF INVENTION: DNA CODING THEREFOR
 : NUMBER OF SEQUENCES: 23
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P. L. L. C.
 : STREET: 1200 G Street, N. W., Suite 700
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20005
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-430-56

```

```

Query Match          36.7%; Score 264; DB 4; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.3e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

```

```

QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELECVPTGQHVNRQILMIR-YPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :
DB 72 IFKPSCVPLMRGCGCCNDEGLECVPTESNITMQIMIRKPHQGHIGEMSLFQHNKCECR 131
QY 126 PKK 128
   |||
DB 132 PKK 134

```

```

RESULT 27
US-09-392-932-3
; Sequence 3, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-392-932-3

```

```

Query Match          36.7%; Score 264; DB 4; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.3e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

```

```

QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELECVPTGQHVNRQILMIR-YPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :

```

```

DB 72 IFKPSCVPLMRGCGCCNDEGLECVPTESNITMQIMIRKPHQGHIGEMSLFQHNKCECR 131
QY 126 PKK 128
   |||
DB 132 PKK 134

```

```

RESULT 28
5332671-4
; Patent No. 5332671
; APPLICANT: FERRARA, NAPOLEONE; LEUNG, DAVID W.H.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,722
; FILING DATE: 04-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 369,424
; FILING DATE: 21-JUN-1989
; APPLICATION NUMBER: 351,117
; FILING DATE: 12-MAY-1989
; SEQ ID NO:4
; LENGTH: 191
; 5332671-4

```

```

Query Match          36.7%; Score 264; DB 6; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.3e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

```

```

QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELECVPTGQHVNRQILMIR-YPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :
DB 72 IFKPSCVPLMRGCGCCNDEGLECVPTESNITMQIMIRKPHQGHIGEMSLFQHNKCECR 131
QY 126 PKK 128
   |||
DB 132 PKK 134

```

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RESULT 29
5240848-11
; Patent No. 5240848
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; PEDER, JOSEPH
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/337,037
; FILING DATE: 10-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 274,061
; FILING DATE: 21-NOV-1988
; SEQ ID NO:11
; LENGTH: 214
; 5240848-11

```

```

Query Match          36.7%; Score 264; DB 6; Length 214;
Best Local Similarity 43.9%; Pred. No. 1.5e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

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QY 10 LALLQLAPQAQAVSQPDAG---HQRKYVSWIDYTRATCQPREVVVPLTVELMGTVAK 66
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LALLLYLHNAKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDELECVPTGQHVNRQILMIR-YPSSQLGEMSLSEHSQCECR 125
   ||||| : ||||| : ||||| : : : : : : : : : : : : : : : : : : : :

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Dd	72	1FKFSQVPLMKCGGCCNDEGLECYPTESNITWQIMRIKPHQGIGBMSFLQHNKCECR	133
Qy	126	PKK	128
Dd	132	PKK	134

RESULT 30
US-08-807-992B-3
; Sequence 3, Application US/08807992B
; Patent No. 6022541

```

: GENERAL INFORMATION:
:
: APPLICANT: Senger, Donald R
:
: APPLICANT: Dvorak, Harold F
:
: TITLE OF INVENTION: Immunological preparation for concurrent
:
: TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
:
: TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
:
: TITLE OF INVENTION: vessel
:
: NUMBER OF SEQUENCES: 31

```

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
3
4 COMPUTER: IBM PS/1
5
6 OPERATING SYSTEM: MS DOS
7
8 SOFTWARE: Wordperfect version 5.1
9
10 CURRENT APPLICATION DATA:
11
12 APPLICATION NUMBER: US/08/807,992B
13
14 FILING DATE: March 3, 1997

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Query Match	36.7%	Score 264	DB 3	length 215
Best Local Similarly	43.98%	Pred. No. 1.5e-23		
Matches 54	Conservative 21	Mismatches 44	Indels 4	Gaps 2

[illegible]

RESULT 31
US-08-586-039B-49
; Sequence 49, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION: ~
; APPLICANT: Bayne, Marvin L.

```

; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
;
; TITLE OF INVENTION: SUBUNIT
;
; NUMBER OF SEQUENCES: 49
;
; CORRESPONDENCE ADDRESS:
;

```

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: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC Compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Microsoft Word 6
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/586,039B
:
: FILING DATE: 16-JAN-1996

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Query Match	36.7%	Score 264	DR 4	Length 215
Best Local Similarity	43.9%	Pred. No. 1.5e-23		
Matches 54	Conservative 21	Mismatches 44	Indels 4	Gaps 2

[illegible]

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RESULT 32
5240848-7
PATENT NO. 5240848
APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH
TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR
PERMEABILITY FACTOR HAVING 189 AMINO ACIDS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/337,037
FILING DATE: 10-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 274,061
FILING DATE: 21-NOV-1988
SEQ ID NO.: 7
LENGTH: 215

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: IBM PS/1
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,992B
FILING DATE: March 3, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-807-992B-4

Query Match 36.7%; Score 264; DB 3; Length 232;
Best Local Similarity 43.9%; Pred. No. 1.6e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;
DB 10 LAALLQAPAPVSDPAPG---HQRKVVSMIDYTRATCOPREVVVPLTVELMGTVAK 66
12 LALLLYLHNAKWSQAPAPMAGGGGQNHHEVVKFMDYVQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDGECVPTGQHOVMOJLMIR-YPSOLGEMSLSEHSQCCECR 125
DB 72 IKFPCSVPLMRGCGCNDGECVPTESNITMQIMRIKPHQGQIHGEMSFQHNKCECR 131
QY 126 PRK 128
DB 132 PRK 134

RESULT 36
US-09-042-105-7
Sequence 7, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968

FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-042-105-7

Query Match 36.7%; Score 264; DB 3; Length 232;
Best Local Similarity 43.9%; Pred. No. 1.6e-23;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;
DB 10 LAALLQAPAPVSDPAPG---HQRKVVSMIDYTRATCOPREVVVPLTVELMGTVAK 66
12 LALLLYLHNAKWSQAPAPMAGGGGQNHHEVVKFMDYVQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDGECVPTGQHOVMOJLMIR-YPSOLGEMSLSEHSQCCECR 125
DB 72 IKFPCSVPLMRGCGCNDGECVPTESNITMQIMRIKPHQGQIHGEMSFQHNKCECR 131
QY 126 PRK 128
DB 132 PRK 134

RESULT 37
5219739-22
Patent No. 5219739
APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
JOHN C.; MITCHELL, RICHARD L.
TITLE OF INVENTION: DNA SEQUENCES ENCODING BVESGF120 AND
HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVESGF120 AND HVEGF121
NUMBER OF SEQUENCES: 40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/559,041
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
SEQ ID NO:22:
LENGTH: 215
5219739-22

Query Match 36.6%; Score 263; DB 6; Length 215;
Best Local Similarity 43.1%; Pred. No. 2e-23;
Matches 53; Conservative 22; Mismatches 44; Indels 4; Gaps 2;
DB 10 LAALLQAPAPVSDPAPG---HQRKVVSMIDYTRATCOPREVVVPLTVELMGTVAK 66
12 LALLLYLHNAKWSQAPAPMAGGGGQNHHEVVKFMDYVQRSYCHPIETLVDFQEPDEIEY 71
QY 67 QLVPSCVTVQRCGCCPDDGECVPTGQHOVMOJLMIR-YPSOLGEMSLSEHSQCCECR 125
DB 72 IKFPCSVPLMRGCGCNDGECVPTESNITMQIMRIKPHQGQIHGEMSFQHNKCECR 131

OY 126 PRK 128
Db 132 PRK 134

RESULT 38

US-08-691-794-3
; Sequence 3, Application US/08691794
; Patent No. 6057428

GENERAL INFORMATION:

APPLICANT: Keyt, Bruce A.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
APPLICANT: Cunningham, Brian C.
APPLICANT: Wells, James A.

APPLICANT: L. Bing

TITLE OF INVENTION: Variants of Vascular Endothelial Cell

TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their

TITLE OF INVENTION: Production

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flehr, Hobach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/691,794

FILING DATE: 02-AUG-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,827

FILING DATE: 25-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/567,200

FILING DATE: 05-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-63758/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-691-794-3

Query Match 35.7%; Score 257; DB 3; Length 109;
Best Local Similarity 44.0%; Pred. No. 4.2e-23;
Matches 48; Conservative 21; Mismatches 38; Indels 2; Gaps 2;

OY 21 APVSQDPAPGHQRKRVSMIDVYTRATCPREVVVPLTVELMGTVAKOLVPSCVTVORCG 80
Db 1 APMAEGGGQNH-HEVVFEMDVYQRSYCHPIETLVDFQEVYDELEYIFKPSCVPLMRGCG 59

OY 81 CCPDDGLECVPTGQHOVROMOIMIR-YPPSOLGEMSLSEHSOCECRPK 128
Db 60 CNDGEGLECVPTESNITMOIMRIKPHOGHIGEMSFLOHNKCECRPK 108

RESULT 39

US-09-392-932-11
; Sequence 11, Application US/09392932
; Patent No. 6352975

GENERAL INFORMATION:

APPLICANT: Schreiner, George F.

APPLICANT: Johnson, Richard J.

TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND

TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN

FILE REFERENCE: SCIOS.002A

CURRENT APPLICATION NUMBER: US/09/392,932

CURRENT FILING DATE: 1999-09-09

EARLIER APPLICATION NUMBER: 60/099,694

EARLIER FILING DATE: 1998-09-09

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 110

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-392-932-11

Query Match 35.7%; Score 257; DB 4; Length 110;
Best Local Similarity 44.0%; Pred. No. 4.3e-23;
Matches 48; Conservative 21; Mismatches 38; Indels 2; Gaps 2;

OY 21 APVSQDPAPGHQRKRVSMIDVYTRATCPREVVVPLTVELMGTVAKOLVPSCVTVORCG 80
Db 1 APMAEGGGQNH-HEVVFEMDVYQRSYCHPIETLVDFQEVYDELEYIFKPSCVPLMRGCG 59

OY 81 CCPDDGLECVPTGQHOVROMOIMIR-YPPSOLGEMSLSEHSOCECRPK 128
Db 60 CNDGEGLECVPTESNITMOIMRIKPHOGHIGEMSFLOHNKCECRPK 108

RESULT 40

5194596-19

Patent No. 5194596

APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN

C.; MITCHELL, RICHARD L.

TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL

GROWTH FACTOR

NUMBER OF SEQUENCES: 32

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/450,883

FILING DATE: 14-DEC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 387,545

FILING DATE: 27-JUL-1989

SEQ ID NO:19

LENGTH: 121

5194596-19

Query Match 35.7%; Score 257; DB 6; Length 121;
Best Local Similarity 44.0%; Pred. No. 4.8e-23;
Matches 48; Conservative 21; Mismatches 38; Indels 2; Gaps 2;

OY 21 APVSQDPAPGHQRKRVSMIDVYTRATCPREVVVPLTVELMGTVAKOLVPSCVTVORCG 80
Db 1 APMAEGGGQNH-HEVVFEMDVYQRSYCHPIETLVDFQEVYDELEYIFKPSCVPLMRGCG 59

OY 81 CCPDDGLECVPTGQHOVROMOIMIR-YPPSOLGEMSLSEHSOCECRPK 128
Db 60 CNDGEGLECVPTESNITMOIMRIKPHOGHIGEMSFLOHNKCECRPK 108

RESULT 41
5219739-20
; Patent No. 5219739
; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 00:04:33 : Search time 2004.71 Seconds
(without alignments)
313.161 Million cell updates/sec

Title: US-09-912-436-5_COPY_275_304

Perfect score: 30

Sequence: 1 ctgggggagacgagagtcgagatcc 30

IDENTITY NO 286.94

Gapop, 10.0, Gapext 1.0

Scoring table:

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595303

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 9%

Listing first 45 summaries

Database :
1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_com:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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30: em_hg_hum:*
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32: em_hg_other:*
33: em_hggo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

1	28.4	94.7	202	4	AF099134	AF099134 Bos tauru
2	28.4	94.7	1073	4	AB004274	AB004274 Bos tauru
3	28.4	94.7	1107	4	AB004273	AB004273 Bos tauru
4	26.8	89.3	405	6	AR060514	AR060514 Sequence
5	26.8	89.3	405	6	I36628	I36628 Sequence 8
6	26.8	89.3	565	6	AR060512	AR060512 Sequence
7	26.8	89.3	565	6	I36626	I36626 Sequence 4
8	26.8	89.3	567	10	MMU43837	MMU43837 Mus musculu
9	26.8	89.3	624	6	AR060516	AR060516 Sequence
10	26.8	89.3	795	10	MMU48800	MMU48800 Mus musculu
11	26.8	89.3	886	6	AR060511	AR060511 Sequence
12	26.8	89.3	886	6	I36625	I36625 Sequence 1
13	26.8	89.3	896	10	MMU52820	MMU52820 Mus musculu
14	26.8	89.3	1236	10	MMU43836	MMU43836 Mus musculu
15	26.8	89.3	77265	2	AC099830	AC099830 Homo sapi
16	26.8	89.3	151747	2	AP001453	AP001453 Homo sapi
17	26.8	89.3	174562	10	AC005848	AC005848 Homo sapi
18	25.8	86.0	349	10	AF032925	AF032925 Rattus no
19	25.8	86.0	453	10	AF022952	AF022952 Rattus no
20	23.6	78.7	591	6	AR060513	AR060513 Sequence
21	23.6	78.7	591	6	I36627	I36627 Sequence 6
22	22.6	75.3	87421	2	AC098622	AC098622 Rattus no
23	20.6	68.7	2004	9	BC008593	BC008593 Homo sapi
24	20.6	68.7	6299	9	AB007864	AB007864 Homo sapi
25	20.6	68.7	61633	2	AC084075	AC084075 Homo sapi
26	20.6	68.7	108523	2	AC000159	AC000159 Homo sapi
27	20.6	68.7	135237	2	AP000814	AP000814 Homo sapi
28	20.6	68.7	166269	2	AP001187	AP001187 Homo sapi
29	20.6	68.7	171980	2	AP000928	AP000928 Homo sapi
30	20.6	68.7	178100	2	AP001558	AP001558 Homo sapi
31	20.6	68.7	187483	2	AC090316	AC090316 Homo sapi
32	20.6	68.7	200026	2	AC090368	AC090368 Homo sapi
33	20.4	68.0	41322	9	AC004076	AC004076 Homo sapi
34	20.4	68.0	65870	10	AC005807	AC005807 Mus muscu
35	20.2	67.3	168563	2	AC107025	AC107025 Homo sapi
36	20.2	67.3	178415	2	AC023547	AC023547 Homo sapi
37	20	66.7	3194	9	AB01082501	AB010822 Homo sapi
38	20	66.7	4943	8	CON0180C	CON0180C Homo sapi
39	20	66.7	275272	2	AC097195	AC097195 Rattus no
40	19.6	65.3	258	9	HS157D1R	HS157D1R Homo sapi
41	19.6	65.3	5883	8	AF254143	AF254143 Candida a
42	19.6	65.3	64116	2	AC107940	AC107940 Homo sapi
43	19.6	65.3	110129	9	AC008956	AC008956 Homo sapi
44	19.6	65.3	156641	9	HUAC002544	AC002544 Homo sapi
45	19.6	65.3	166719	9	AC068137	AC068137 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AF099134 202 bp mRNA MAM 05-NOV-2000
DEFINITION Bos taurus vascular endothelial growth factor-B (VEGF-B) mRNA,
partial cds.
ACCESSION AF099134
VERSION AF099134.1 GI:11095133
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 202)
AUTHORS Mandriola, S.J. and Pepper, M.S.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1998) Morphology, CMU, 1 rue Michel Servet, 1211
Geneva 4, Switzerland
FEATURES
source
1..202
/organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="heart"

gene /dev_stage="adult"
<1..>202
/gene="VEGF-B"
<1..>202
CDS /gene="VEGF-B"
/note="flt-1/VEGFR1 ligand"
/codon_start=2
/product="vascular endothelial growth factor-B"
/protein_id="AAC29746.1"
/db_xref="GI:11095134"
/translation="WIDYARATCPREVVPPLMMELMGTVAKOLVPSCVTVQKGGC
CPDGLCEVPRGQVRRQILMT"
BASE COUNT 36 a 59 c 69 g 38 t
ORIGIN

Query Match 94.7%: Score 28.4; DB 4; Length 202;
Best Local Similarity 96.7%: Pred. No. 0.15;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgggcagaccagtcgcgatgcagatcc 30
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Db 165 CTGGGCACACCAAGTCGGAATGCAGATCC 194

RESULT 2
AB004274 1073 bp mRNA linear MAM 12-JAN-2000
LOCUS Bos taurus mRNA for vascular endothelial growth factor B186
DEFINITION precursor, partial cds.
ACCESSION AB004274.1 GI:4850311
VERSION AB004274.1
KEYWORDS vascular endothelial growth factor B186 precursor; vascular endothelial growth factor B186.
SOURCE Bos taurus Heart tissue_l1b:Heart cDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yonekura,H., Sakurai,S., Liu,X., Migita,H., Wang,H., Yamagishi,S., Nomura,M., Abedin,M.J., Unoki,H., Yamamoto,Y. and Yamamoto,H.
TITLE Placenta growth factor and vascular endothelial growth factor B and C expression in microvascular endothelial cells and pericytes.
JOURNAL J. Biol. Chem. 274 (49), 35172-35178 (1999)
MEDLINE 20044783
REFERENCE 2 (bases 1 to 1073)
AUTHORS Liu,X.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1997) Xiaoxu Liu, Kanazawa University School of Medicine, Department of Biochemistry; Takara-machi 13-1, Kanazawa, Ishikawa 920, Japan (E-mail:hyone@med.kanazawa-u.ac.jp, Tel:076-265-2181, Fax:076-234-4226)
FEATURES
source Location/Qualifiers
1..1073
/organism="Bos taurus"
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/tissue_type="Heart"
/tissue_l1b="Heart"
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/codon_start=3
/product="vascular endothelial growth factor B186 precursor"
/protein_id="BAA77686.1"
/db_xref="GI:4850312"
/translation="QLAPQAQVSPQDAPGHQKVVSMIDYARATCPREVVPPLMMELMGTVAKOLVPSCVTVQKGGCPCPDGLCEVPRGQVRRQILMTIYSSQLEMSLEHSDCECRPKRESAVKPRASRPHRPOBRSVPGMDPAPGASPADITHTPTAPGP SAHAPSAASALTPTGPAATAADAAASSVVGGA"
mat_peptide 24..581
BASE COUNT 254 a 354 c 292 g 173 t
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ORIGIN

Query Match 94.7%: Score 28.4; DB 4; Length 1073;
Best Local Similarity 96.7%: Pred. No. 0.14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgggcagaccagtcgcgatgcagatcc 30
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Db 235 CTGGGCACACCAAGTCGGAATGCAGATCC 264

RESULT 3
AB004273 1107 bp mRNA linear MAM 12-JAN-2000
LOCUS Bos taurus mRNA for vascular endothelial growth factor B167
DEFINITION precursor, complete cds.
ACCESSION AB004273.1 GI:4850309
VERSION AB004273.1
KEYWORDS vascular endothelial growth factor B167 precursor; vascular endothelial growth factor B167.
SOURCE Bos taurus Heart tissue_l1b:Heart cDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Yonekura,H., Sakurai,S., Liu,X., Migita,H., Wang,H., Yamagishi,S., Nomura,M., Abedin,M.J., Unoki,H., Yamamoto,Y. and Yamamoto,H.
TITLE Placenta growth factor and vascular endothelial growth factor B and C expression in microvascular endothelial cells and pericytes.
JOURNAL J. Biol. Chem. 274 (49), 35172-35178 (1999)
MEDLINE 20044783
REFERENCE 2 (bases 1 to 1107)
AUTHORS Liu,X.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1997) Xiaoxu Liu, Kanazawa University School of Medicine, Department of Biochemistry; Takara-machi 13-1, Kanazawa, Ishikawa 920, Japan (E-mail:hyone@med.kanazawa-u.ac.jp, Tel:076-265-2181, Fax:076-234-4226)
FEATURES
source Location/Qualifiers
1..1107
/organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="Heart"
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sig_peptide 96..158
CDS 96..662
/codon_start=1
/product="vascular endothelial growth factor B167 precursor"
/protein_id="BAA77685.1"
/db_xref="GI:4850310"
/translation="MSPPLRRLLAVLLQAPQAQVSPQDAPGHQKVVSMIDYARATCPREVVPPLMMELMGTVAKOLVPSCVTVQKGGCPCPDGLCEVPRGQVRRQILMTIYSSQLEMSLEHSDCECRPKRESAVKPRASRPHRPOBRSVPGMDPAPGASPADITHTPTAPGP SAHAPSAASALTPTGPAATAADAAASSVVGGA"
mat_peptide 159..659
BASE COUNT 246 a 368 c 321 g 172 t
ORIGIN

Query Match 94.7%: Score 28.4; DB 4; Length 1107;
Best Local Similarity 96.7%: Pred. No. 0.14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctgggcagaccagtcgcgatgcagatcc 30
|||||
Db 370 CTGGGCACACCAAGTCGGAATGCAGATCC 399

RESULT 4
AR060514 405 bp DNA linear PAT 29-SEP-1999
LOCUS AR060514 Sequence 8 from patent US 5840693.
DEFINITION AR060514
ACCESSION AR060514
VERSION AR060514.1 GI:5986964
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 405)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B
JOURNAL Patent: US 5840693-A 8 24-NOV-1998;
FEATURES
source Location/Qualifiers
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/organism="unknown"

BASE COUNT 93 a 113 c 120 g 79 t
ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.7;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgcagatcc 30
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Db 278 CTGGGCAACACCAAGTCCGAATGCAGATCC 307

RESULT 5
136628 405 bp DNA linear PAT 13-MAY-1997
LOCUS 136628 Sequence 8 from patent US 5607918.
DEFINITION 136628
ACCESSION 136628
VERSION 136628.1 GI:2086453
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 405)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL Patent: US 5607918-A 8 04-MAR-1997;
FEATURES
source Location/Qualifiers
1..405
/organism="unknown"

BASE COUNT 93 a 113 c 120 g 79 t
ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.7;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgcagatcc 30
|||||

Db 278 CTGGGCAACACCAAGTCCGAATGCAGATCC 307

RESULT 6
AR060512 565 bp DNA linear PAT 29-SEP-1999
LOCUS AR060512 Sequence 4 from patent US 5840693.
DEFINITION AR060512
ACCESSION AR060512
VERSION AR060512.1 GI:5986962
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 565)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B

JOURNAL Patent: US 5840693-A 4 24-NOV-1998;
FEATURES
source Location/Qualifiers
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/organism="unknown"

BASE COUNT 120 a 179 c 166 g 100 t
ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.7;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgcagatcc 30
|||||

Db 273 CTGGGCAACACCAAGTCCGAATGCAGATCC 302

RESULT 7
136626 565 bp DNA linear PAT 13-MAY-1997
LOCUS 136626 Sequence 4 from patent US 5607918.
DEFINITION 136626
ACCESSION 136626
VERSION 136626.1 GI:2086451
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 565)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL Patent: US 5607918-A 4 04-MAR-1997;
FEATURES
source Location/Qualifiers
1..565
/organism="unknown"

BASE COUNT 120 a 179 c 166 g 100 t
ORIGIN

Query Match 89.3%; Score 26.8; DB 6; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.7;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatgcagatcc 30
|||||

Db 273 CTGGGCAACACCAAGTCCGAATGCAGATCC 302

RESULT 8
MMU43837 567 bp mRNA linear ROD 16-MAY-1996
LOCUS MMU43837
DEFINITION Mus musculus VEGF-related factor mvrfl67 precursor mRNA, complete cds.
ACCESSION U43837
VERSION U43837.1 GI:1314335
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 567)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Townson,S., Lagercrantz,J., Grimmond,S., Silins,G., Nordenskjold,M., Weber,G. and Hayward,N.
JOURNAL Characterization of the murine VEGF-related factor gene
MEDLINE Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
REFERENCE 96183052
2 (bases 1 to 567)
AUTHORS Hayward,N.K.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental
Oncology Unit, Queensland Institute of Medical Research, Bancroft
Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029,
Australia
FEATURES
Location/Qualifiers

	source	1..567 /organism="Mus musculus" /db_xref="taxon:10090" /clone="m175.m1" /tissue_type="whole brain" /clone_lib="Stratagene unizap neonatal whole brain cdna library" /dev_stage="neonatal"
CDS		1..567 /note="VEGF-related factor isoform" /codon_start=1 /product="mvrlf67" /protein_id="AAC52553.1" /db_xref="GI:1314336" /translation="MSPLLRRLILVALIQLARQAPVSGFDPSSHOKKVPYMDIVARATCPREVVYPPLSMELMGNYKKQIYPSGVYQRGGCCPDGLGTCYPRGGHGYVKQIIIMIQIPSSQLGEMSLSEHSQCRCRKKEAVKPSPRIICPCTQRORPPTRCRCCRRLFLHCGRGLELNDPTCRCRRPK" 61..564 /note="VEGF-related factor isoform" /product="mvrlf67"
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Matches	28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	1 ctgggcagcaccgaagtccggtacgatcc 30 Db 275 CTGGGCACACCAGTCCGAATGCAGATCC 304	
RESULT 3		
LOCUS	AR060516 624 bp DNA linear PAT 29-SEP-1999	
DEFINITION	Sequence 12 from patent US 5840693.	
ACCESSION	AR060516	
VERSION	AR060516.1 GI:5986966	
KEYWORDS	.	
SOURCE	Unknown. Unclassified.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 624) Eriksson,U.A., Olofsson,B., Alltalo,K. and Pajusola,K. Vascular endothelial growth factor-B Patent: US 5840693-A 12-24-NOV-1998; Location/Qualifiers 1..624	
FEATURES	Source	
BASE COUNT	124 a 213 c 173 g 114 t	
ORIGIN		
Query Match	89.3%; Score 26.8; DB 6; Length 624;	
Best Local Similarity	93.3%; Pred. No. 0.7;	
Matches	28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	1 ctgggcagcaccgaagtccggtacgatcc 30 Db 275 CTGGGCACACCAGTCCGAATGCAGATCC 304	
RESULT 13		
LOCUS	MMU48800 795 bp mRNA linear ROD 19-AUG-1996	
DEFINITION	Mus musculus vascular endothelial growth factor B precursor	
ACCESSION	U48800	
VERSION	U48800.1 GI:1234824	
KEYWORDS	. house mouse.	

ORGANISM	Mus musculus
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Mus.
AUTHORS	1 (bases 1 to 795)
TITLE	Olofsson, B., Pajusola, K., Kaipainen, A., von Euler, G., Joukov, V., Saksela, O., Orpana, A., Pettersson, R. F., Alltalo, K. and Eriksson, U. Vascular endothelial growth factor B, a novel growth factor for endothelial cells
JOURNAL	Proc Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
MEDLINE	9619755
REFERENCE	2 (bases 1 to 795)
AUTHORS	Eriksson, U., Olofsson, B., Alltalo, K. and Pajusola, K.
TITLE	Direct Submission
JOURNAL	Submitted (08-FEB-1996) Ulf Eriksson, Ludwig Institute for Cancer Research, Karolinska Institutet, Doktorsringen 12A, Stockholm, S-171 77, Sweden
FEATURES	Location/Qualifiers
source	1..795
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	/db_xref="taxon:10090"
	/tissue_type="heart"
	/dex_stage="adult"
gene	1..795
	/gene="VEGF-B"
CDS	95..661
	/gene="VEGF-B"
	/note="forms disulfide linked homodimers; forms disulfide linked heterodimers with VEGF; binds heparin"
	/codon_start=1
	/product="vascular endothelial growth factor B precursor"
	/protein_id="AA06273.1"
	/db_xref="GI:1234825"
	/translation="MSPDLRLVALLQLARTQAPVSDGSPSHOKKVPVWIDVYAR
	ATCPREVVPLSMELGNVYKOLVPCSVYVQSGCGCPDGLCVPTGOHVMQTL
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sig_peptide	95..157
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mat_peptide	158..658
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BASE COUNT	154 a 270 c 234 g 137 t
ORIGIN	
Query Match	89.3%; Score 26.8; DB 10; Length 795;
Best Local Similarity	93.3%; Pred. No. 0.69;
Matches	28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
0y	1 ctgggcagaccgaatccgcatgcagatcc 30
Db	369 CTGGGCACACCAAGTCCGAATGCAGATCC 398
RESULT 11	
LOCUS	AR060511 886 bp DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 1 from patent US 5840693.
ACCESSION	AR060511
VERSION	AR060511.1
KEYWORDS	GI:5986961
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 886)
AUTHORS	Eriksson, U., Olofsson, B., Alltalo, K. and Pajusola, K.
TITLE	Vascular endothelial growth factor-B
JOURNAL	Patent: US 5840693-A 1 24-NOV-1998;
FEATURES	Location/Qualifiers
source	1..886
	/organism="unknown"
BASE COUNT	227 a 261 c 226 g 172 t
ORIGIN	

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Query Match      89.3%; Score 26.8; DB 6; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacacagtcgagtcgagatcc 30
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Db 184 CTGGGCACACACCAAGTCGATGCGATCC 213

RESULT 12
LOCUS 136625 886 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5607918.
ACCESSION 136625
VERSION 136625.1 GI:2086450
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 886)
  Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
  TITLE Vascular endothelial growth factor-B and DNA coding therefor
  JOURNAL Patent: US 5607918-A 1 04-MAR-1997;
  FEATURES
    location/Qualifiers
      source 1..886 /organism="unknown"

BASE COUNT 227 a 261 c 226 g 172 t
ORIGIN

Query Match      89.3%; Score 26.8; DB 6; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacacagtcgagtcgagatcc 30
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Db 184 CTGGGCACACACCAAGTCGATGCGATCC 213

RESULT 13
LOCUS MMU52820 896 bp mRNA linear ROD 08-OCT-1996
DEFINITION Mus musculus vascular endothelial growth factor B 186 (VEGF-B)
ACCESSION MMU52820
VERSION U52820.1 GI:1488260
KEYWORDS
SOURCE
ORGANISM house mouse.
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 896)
  Olofsson,B., Pajusola,K., Kaipainen,A., von Euler,G., Joukov,V.,
  Saksela,O., Orpana,A., Petersson,R.F., Allitalo,K. and Eriksson,U.
  TITLE Vascular endothelial growth factor B, a novel growth factor for
  endothelial cells
  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
  MEDLINE 96197355
  REFERENCE 2 (bases 1 to 896)
  Olofsson,B., Pajusola,K., von Euler,G., Chliov,D., Allitalo,K. and
  Eriksson,U.
  TITLE Genomic organization of the mouse and human genes for vascular
  endothelial growth factor B (VEGF-B) and characterization of a
  second splice isoform
  J. Biol. Chem. 271 (32), 19310-19317 (1996)
  MEDLINE 96325041
  REFERENCE 3 (bases 1 to 896)
  Eriksson,U., Allitalo,K., Olofsson,B. and Pajusola,K.
  TITLE Direct Submission
  JOURNAL Submitted (27-MAR-1996) Ulf Eriksson, Ludwig Institute for Cancer
  Research, Karolinska Institutet, Doktorsringen 12A, Stockholm S-171

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77, Sweden
FEATURES
  source
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      /db_xref="taxon:10090"
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      /gene="VEGF-B"
      95..718
      /gene="VEGF-B"
      /codon_start=1
      /product="vascular endothelial growth factor B 186"
      /protein_id="AAC52823.1"
      /db_xref="GI:1488261"
      /translation="MSPLLRRLVALLQLARQAPVSGDFGSHQKRVVPIDVYAR
      ATCPREVVPVPLSMELMGNVKOLVPCSVVORCGCCPDGLEGVPTGQHOVMQTL
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BASE COUNT 170 a 317 c 254 g 155 t
ORIGIN

Query Match      89.3%; Score 26.8; DB 10; Length 896;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcgacacacacagtcgagtcgagatcc 30
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Db 369 CTGGGCACACCAAGTCGATGCGATCC 398

RESULT 14
LOCUS MMU43836 1236 bp mRNA linear ROD 04-DEC-1996
DEFINITION Mus musculus VEGF-related factor mvrf186 precursor mRNA, complete
  cds.
ACCESSION U43836
VERSION U43836.1 GI:1703480
KEYWORDS
SOURCE
ORGANISM house mouse.
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 1236)
  Townsend,S., Lagercrantz,J., Gimmond,S., Sillins,G.,
  Nordenskjold,M., Weber,G. and Hayward,N.
  TITLE Characterization of the murine VEGF-related factor gene
  Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
  MEDLINE 96183052
  REFERENCE 2 (bases 1 to 1236)
  Hayward,N.K.
  TITLE Direct Submission
  JOURNAL Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental
  Oncology Unit, Queensland Institute of Medical Research, Bancroft
  Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029,
  Australia
  On Dec 4, 1996 this sequence version replaced gi:1314333.
  COMMENT Location/Qualifiers
    1..1236
    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /clone="m175-m1"
    /tissue_type="whole brain"
    /clone_lib="Stratagene unizap neonatal whole brain cDNA
    library"
    /dev_stage="neonatal"
    193..816
    /note="VEGF-related factor"
    /codon_start=1
    /product="mvrf186 precursor"
    /protein_id="AAC52932.1"
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mat_peptide /translation="NSPLLRLLLVALLDLARTQADVPQDFGDSHQKKVVPIDVYAR
ATCQPREVVVPLSMELMGNVVKQVPSVYVRCGGCCPDGDECVTQGHVYRMQIL
MIQYPSQIGEMSLERHSQCEKPKRSKSAVKPDRAIPHHRQPSVYCGMDSTPCAS
SPADIIHPPIPPAPSSARLAPSAVNALTPGPAADAAAADAAASIAKGA"

256. 813
/note="VBSG-related factor"
/product="mvrf186"

BASE COUNT 240 a 429 c 340 g 227 t
ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 1236;
Best Local Similarity 93.3%; Pred. No. 0.69;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctgagcagcaccacagtcgcagtcagatcc 30
||||| ||||||| ||||||| |||||||
Db 467 CTGGGCAACACCAAGTCGATCGAGATCC 496

RESULT 15
AC099830 77265 bp DNA linear HTG 22-NOV-2001
LOCUS Homo sapiens chromosome 11 clone RP11-783K16 map 11, LOW-PASS
DEFINITION
SEQUENCE SAMPLING.
AC099830
AC099830.1 GI:17047170
VERSION
KEYWORDS HTG: HTGS_PHASE0.
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., and Lander,E.
TITLE 1 (bases 1 to 77265)
JOURNAL Homo sapiens chromosome 11, clone RP11-783K16
REFERENCE 2 (bases 1 to 77265)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barina,N., Bastien,V., Boguslavsky,L., Bouhgalter,B.,
Brown,A., Camarata,J., Campolano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferro,S.,
Freire,P., Fitzhugh,W., Gage,D., Galagan,J., Gaidyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
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Maclean,C., MacDonald,P., Major,J., Margulis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrum,T.,
Meneus,L., Mlnova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Plerre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schnupack,R.,
Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigillo,J., Vassiliev,I.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 520 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12600
Center clone name: 783_K_16

NOTE: This record contains 79 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
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837: contig of 837 bp in length
838 937: gap of 100 bp
938 1807: contig of 870 bp in length
1808 1907: gap of 100 bp
1908 2811: contig of 904 bp in length
2812 2911: gap of 100 bp
2912 3812: contig of 901 bp in length
3813 3912: gap of 100 bp
3913 4754: contig of 842 bp in length
4755 4854: gap of 100 bp
4855 5710: contig of 856 bp in length
5711 5810: gap of 100 bp
5811 6694: contig of 884 bp in length
6695 6794: gap of 100 bp
6795 7715: contig of 921 bp in length
7716 7815: gap of 100 bp
7816 8681: contig of 866 bp in length
8682 8781: gap of 100 bp
8782 9652: contig of 871 bp in length
9653 9752: gap of 100 bp
9753 10637: contig of 885 bp in length
10638 10737: gap of 100 bp
10738 11596: contig of 859 bp in length
11597 11696: gap of 100 bp
11697 12630: contig of 934 bp in length
12631 12730: gap of 100 bp
12731 13658: contig of 928 bp in length
13659 13758: gap of 100 bp
13759 14651: contig of 893 bp in length
14652 14751: gap of 100 bp
14752 15639: contig of 888 bp in length
15640 15739: gap of 100 bp
15740 16616: contig of 877 bp in length
16617 16716: gap of 100 bp
16717 17590: contig of 874 bp in length
17591 17690: gap of 100 bp
17691 18640: contig of 950 bp in length
18641 18740: gap of 100 bp
18741 19606: contig of 866 bp in length
19607 19706: gap of 100 bp
19707 20586: contig of 880 bp in length
20587 20686: gap of 100 bp
20687 21608: contig of 922 bp in length
21609 21708: gap of 100 bp
21709 22606: contig of 898 bp in length
22607 22706: gap of 100 bp
22707 23613: contig of 907 bp in length
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24560 24659: gap of 100 bp
24660 25529: contig of 870 bp in length
25530 25629: gap of 100 bp
25630 26489: contig of 860 bp in length
26490 26589: gap of 100 bp
26590 27485: contig of 896 bp in length
27486 27585: gap of 100 bp
27586 28437: contig of 852 bp in length
28438 28537: gap of 100 bp
28538 29418: contig of 881 bp in length
29419 29518: gap of 100 bp
29519 30409: contig of 891 bp in length


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* 30410 30509: gap of 100 bp
* 30510 31404: contig of 895 bp in length
* 31405 31504: gap of 100 bp
* 31505 32396: contig of 892 bp in length
* 32397 32496: gap of 100 bp
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* 34448 35330: contig of 883 bp in length
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* 39317 40227: contig of 911 bp in length
* 40228 40327: gap of 100 bp
* 40328 41227: contig of 900 bp in length
* 41228 41327: gap of 100 bp
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* 57770 58674: contig of 905 bp in length
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* 59769 60677: contig of 909 bp in length
* 60678 60777: gap of 100 bp
* 60778 61629: contig of 852 bp in length
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* 62690 63545: contig of 856 bp in length
* 63546 63645: gap of 100 bp
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* 65576 66464: contig of 889 bp in length
* 66465 66564: gap of 100 bp
* 66565 67430: contig of 866 bp in length
Query Match 89.3%; Score 26.8; DB 2; Length 77265;
Best local similarity 93.3%; Pred. No. 0.66;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 ctggcagcaccagtcgcgatgcagatcc 30
Db 55148 CTGGCAGCACCAAGTCCGATCGAGTAC 55177

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RESULT 16

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AP001453 151747 bp DNA linear HTG 14-SEP-2000
LOCUS Homo sapiens chromosome 11 clone RP11-783K16 map 11q13, WORKING
DEFINITION DRAFT SEQUENCE, 37 unordered pieces.
ACCESSION AP001453
VERSION AP001453.3 GI:10130047
KEYWORDS HTG; HTGS-PARSE1; HTGS-DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-783K16.
ORGANISM Homo sapiens

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REFERENCE 1 (bases 1 to 151747)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

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TITLE Homo sapiens 151,747 genomic DNA of 11q13
JOURNAL Published Only in Database (2000) In press
REFERENCE 2 (bases 1 to 151747)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

```

```

TITLE Submitted (15-MAR-2000) Masahira Hattori, The Institute of Physical
JOURNAL and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan

```

```

COMMENT (E-mail:hattori@gs.riken.go.jp, URL:http://hnp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Sep 15, 2000 this sequence version replaced g1:8117327.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)

```

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Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gs.riken.go.jp
----- Project Information
Center project name: HumDra111
Center clone name: RP11-783K16
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 136959 bases at least Q40
Consensus quality: 143151 bases at least Q30
Consensus quality: 146210 bases at least Q20
Insert size: 148147, sum-of contigs
Quality coverage: 8.32x in Q20 bases; sum-of contigs
-----

```

```

NOTE: This is a 'working draft' sequence. It currently consists of
37 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

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1 8902 contig of 8902 bp in length
9003 18232 contig of 9230 bp in length
18333 28659 contig of 10337 bp in length
28760 37331 contig of 8572 bp in length
37432 45066 contig of 7635 bp in length
45167 51737 contig of 6571 bp in length
51838 57917 contig of 6080 bp in length
58018 62697 contig of 4680 bp in length

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62798 66342 contig of 3545 bp in length
66443 69246 contig of 2804 bp in length
69347 72173 contig of 2827 bp in length
72274 76432 contig of 4159 bp in length
76533 80848 contig of 4316 bp in length
80949 84529 contig of 3581 bp in length
84630 88588 contig of 3959 bp in length
88689 94224 contig of 5536 bp in length
94325 98727 contig of 4403 bp in length
98828 102160 contig of 3333 bp in length
102261 107715 contig of 5455 bp in length
107816 114480 contig of 3665 bp in length
114581 117720 contig of 3585 bp in length
117821 121176 contig of 3356 bp in length
121277 123962 contig of 2686 bp in length
124063 128424 contig of 4362 bp in length
128525 131281 contig of 2756 bp in length
131381 133765 contig of 2384 bp in length
133865 137167 contig of 3302 bp in length
137267 139968 contig of 2702 bp in length
140069 141380 contig of 1312 bp in length
141481 142715 contig of 1235 bp in length
142816 144247 contig of 1432 bp in length
144348 146023 contig of 1675 bp in length
146123 147417 contig of 1294 bp in length
147517 148926 contig of 1410 bp in length
149027 150172 contig of 1146 bp in length
150273 151747 contig of 1475 bp in length.

NOTE: This is a 'working draft' sequence. It currently
consists of 37 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved. 8902: contig of 8902 bp in length
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8903 9002: gap of 100 bp
9003 18232: contig of 9230 bp in length
18233 18332: gap of 100 bp
18333 28659: contig of 10327 bp in length
28660 28759: gap of 100 bp
28760 37331: contig of 8572 bp in length
37332 37431: gap of 100 bp
37432 45066: contig of 7635 bp in length
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45167 51737: contig of 6571 bp in length
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69347 72173: contig of 2827 bp in length
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72274 76432: contig of 4159 bp in length
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98828 102160: contig of 3333 bp in length
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* 107716 107815: gap of 100 bp
* 107816 114480: contig of 3665 bp in length
* 114581 117720: gap of 100 bp
* 11581 11580: gap of 100 bp
* 11581 114035: contig of 2455 bp in length
* 114036 114135: gap of 100 bp
* 114136 117720: contig of 3585 bp in length
* 11721 117820: gap of 100 bp
* 117821 121176: contig of 3356 bp in length
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* 121277 123962: contig of 2686 bp in length
* 123963 124062: gap of 100 bp
* 124063 128424: contig of 4362 bp in length
* 128425 128524: gap of 100 bp
* 128525 131280: contig of 2756 bp in length
* 131281 131380: gap of 100 bp
* 131381 133764: contig of 2384 bp in length
* 133765 133864: gap of 100 bp
* 133865 137166: contig of 3302 bp in length
* 137167 137266: gap of 100 bp
* 137267 139968: contig of 2702 bp in length
* 139969 140068: gap of 100 bp
* 140069 141380: contig of 1312 bp in length
* 141381 141480: gap of 100 bp
* 141481 142715: contig of 1235 bp in length
* 142716 142815: gap of 100 bp
* 142816 144247: contig of 1432 bp in length
* 144248 144347: gap of 100 bp
* 144348 146022: contig of 1675 bp in length
* 146023 146122: gap of 100 bp
* 146123 147416: contig of 1294 bp in length
* 147417 147516: gap of 100 bp
* 147517 148926: contig of 1410 bp in length
* 148927 149026: gap of 100 bp
* 149027 150172: contig of 1146 bp in length
* 150173 150272: gap of 100 bp
* 150273 151747: contig of 1475 bp in length.

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      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="11"
      /map="11q13"
      /clone="RP11-783K16"
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      9003..18232
      /note="assembly_fragment"
      18333..28659
      /note="assembly_fragment"
      28760..37331
      /note="assembly_fragment"
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Query Match 89.3%; Score 26.8; DB 2; Length 151747;
Best Local Similarity 93.3%; Pred. No. 0.65;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY      1  ctgggacgaccgaagtcggatgcagatcc 30
Db 148127 CTGGGACAGCACCAGTCGGATGCAGGTAC 148156

RESULT 17
AC005848/c
LOCUS   Homo sapiens chromosome 11 clone CIT987SK-1012F4, *** SEQUENCING IN
DEFINITION
ACCESSION AC005848
VERSION   AC005848.1 GI:3779014
KEYWORDS  HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL   1 (bases 1 to 174562)
TITLE     Smith,D.R.
REFERENCE Sequencing of Human Chromosome 10
AUTHORS   2 (bases 1 to 174562)
JOURNAL   Smith,D.R.
REFERENCE Direct Submission
AUTHORS   Submitted (22-OCT-1998) Genome Therapeutics Corporation, 100 Beaver
JOURNAL   Street, Waltham, MA 02154, USA
COMMENT   * NOTE: This is a 'working draft' sequence. It currently
          * consists of 6 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *
          * 1 4561: contig of 4561 bp in length
          * 4562 19077: gap of unknown length
          * 19078 30350: contig of 11273 bp in length
          * 30351 44866: gap of unknown length
          * 44867 58909: contig of 14043 bp in length
          * 58910 73424: gap of unknown length
          * 73425 90412: contig of 16988 bp in length
          * 90413 104927: gap of unknown length
          * 104928 130554: contig of 25627 bp in length
          * 130555 145068: gap of unknown length
          * 145070 174562: contig of 29493 bp in length.
          *
          * Location/Qualifiers
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              /db_xref="taxon:9606"
              /chromosome="11"
              /clone="CIT987SK-1012F4"
              /db_xref="taxon:1012F4"

BASE COUNT 21150 a 29998 c 29519 g 21315 t 72580 others
ORIGIN
Query Match      89.3%; Score 26.8; DB 2; Length 174562;
Best Local Similarity 93.3%; Pred. No. 0.65;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1  ctgggacgaccgaagtcggatgcagatcc 30
Db 29612 CTGGGACAGCACCAGTCGGATGCAGGTAC 29583

RESULT 18
AF032925
LOCUS   Rattus norvegicus vascular endothelial growth factor B 186
DEFINITION
ACCESSION AF032925
VERSION   AF032925.1 GI:2641621
KEYWORDS

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SOURCE      Norway rat.
ORGANISM    Rattus norvegicus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
JOURNAL     Rattus.
TITLE       1 (bases 1 to 349)
REFERENCE   Mandriota,S.J. and Pepper,M.S.
AUTHORS     Direct Submission
JOURNAL     Submitted (03-NOV-1997) Morphology, University Medical Center, 1
TITLE       rue Michel Servet, 1211 Geneva 4, Switzerland
REFERENCE   Location/Qualifiers
AUTHORS     1..349
JOURNAL     /organism="Rattus norvegicus"
TITLE       /strain="Sprague-Dawley"
REFERENCE   /db_xref="taxon:10116"
AUTHORS     /tissue_type="placenta"
JOURNAL     /note="RT-PCR product amplified from total RNA from rat
TITLE       placenta, using degenerate oligonucleotides; sequenced on
REFERENCE   both strands"
AUTHORS     <1..349
JOURNAL     /note="vascular endothelial growth factor-related factor
TITLE       (VRP) 186 precursor; VEGF-B 186 precursor"
REFERENCE   /codon_start=2
AUTHORS     /product="vascular endothelial growth factor B 186
JOURNAL     precursor"
TITLE       /protein_id="AAB86884.1"
REFERENCE   /db_xref="GI:2641622"
AUTHORS     /translation="EVVPLSMELGNVNVQLVPSCVTVORGCCPDGLGCVPIGO
JOURNAL     HOVMQIMIOYPSOIGSEMSLEHSCCECRPKRESAVRPFVAIPHHRPQPSVLS
TITLE       WDSAPGSSPADIT"
AUTHORS     MDSAPGSSPADIT"

BASE COUNT  78 a 99 c 104 g 68 t
ORIGIN
Query Match      86.0%; Score 25.8; DB 10; Length 349;
Best Local Similarity 93.1%; Pred. No. 1.9;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2  tgggacgaccgaagtcggatgcagatcc 30
Db 127 TGGGACAGCACCAGTCGGATGCAGGTAC 155

RESULT 19
AF022952
LOCUS   Rattus norvegicus vascular endothelial growth factor B mRNA,
DEFINITION partial cds.
ACCESSION AF022952
VERSION   AF022952.1 GI:2766601
KEYWORDS
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
JOURNAL     Rattus.
TITLE       1 (bases 1 to 453)
REFERENCE   Well,J., Eschenhagen,T., Mittmann,C. and Scholz,H.
AUTHORS     Isolation and characterization of rat vascular endothelial growth
JOURNAL     factor B (VEGF-B)
TITLE       unpublished
REFERENCE   2 (bases 1 to 453)
AUTHORS     Well,J., Eschenhagen,T., Mittmann,C. and Scholz,H.
JOURNAL     Direct Submission
TITLE       Submitted (31-AUG-1997) Abteilung Allgemeine Pharmakologie,
REFERENCE   Universitaets-Krankenhaus Eppendorf, Martinstr.52, Hamburg 20246,
JOURNAL     Germany

```

```

FEATURES
SOURCE      Location/Qualifiers
            1..453
              /organism="Rattus norvegicus"
              /db_xref="taxon:10116"
              /tissue_type="heart"
              /note="isolated by PCR"

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CDS

<1..>453
/note="VEGF-B"
/codon_start=2
/product="vascular endothelial growth factor B"
/protein_id="AAB95447.1"
/db_xref="GI:2766602"
/translation="KRKYSVMDIVARATCGREVVVPSMEPMGVNVPKQFVPSCTV
QKGGCCPDGECVPIGQVYRMQIMTQYSSQLGEMSLSEHSQCRCRPRKESAV
KPDSPRTLCPTXRXRPDPTRCRCRRRRFLHCQGLGLNPDTC"
BASE COUNT 105 a 126 c 136 g 84 t 2 others
ORIGIN

Query Match 86.0%; Score 25.8; DB 10; Length 453;
Best Local Similarity 93.1%; Pred. No. 1.9;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 tgggcagaccacgaatccgagtcagatcc 30
Db 184 TGGGCAACACCAAGTCCGAATGCAGATCC 212

RESULT 20
LOCUS AR060513 591 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5840693.
ACCESSION AR060513
VERSION AR060513.1 GI:5986963
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 591)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B
JOURNAL Patent: US 5840693-A 6 24-NOV-1998;
FEATURES
Location/Qualifiers
source 1..591

BASE COUNT 126 a 186 c 174 g 105 t
ORIGIN

Query Match 78.7%; Score 23.6; DB 6; Length 591;
Best Local Similarity 86.7%; Pred. No. 16;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctgggcagaccacgaatccgagtcagatcc 30
Db 278 CTGGGCAACACCAAGTCCGAATGCAGGTAC 307

RESULT 21
LOCUS 136627 591 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 6 from patent US 5607918.
ACCESSION I36627
VERSION I36627.1 GI:2086452
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 591)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL Patent: US 5607918-A 6 04-MAR-1997;
FEATURES
Location/Qualifiers
source 1..591

BASE COUNT 126 a 186 c 174 g 105 t
ORIGIN

Query Match 78.7%; Score 23.6; DB 6; Length 591;
Best Local Similarity 86.7%; Pred. No. 16;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctgggcagaccacgaatccgagtcagatcc 30
Db 278 CTGGGCAACACCAAGTCCGAATGCAGGTAC 307

RESULT 22
LOCUS AC098622/c 87421 bp DNA linear HTG 20-DEC-2001
DEFINITION Rattus norvegicus clone CH230-92M16, *** SEQUENCING IN PROGRESS
AC098622
AC098622.3 GI:17973410
VERSION HTG: HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 87421)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C., Alstrooms,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhaay,C., Burch,P., Burkett,S., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Drepper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frenzel,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Hollaway,C., Hollins,B., Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvan,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S., Ogun,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonalke,J., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Teifrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,A., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zortilla,S., Nelson,D., Weinstein,G. and Glibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 87421)
Worley,K.C.
Submitted (27-Oct-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064359.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Center: Baylor College of Medicine

Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc.helpebcm.tmc.edu
----- Project Information
Center project name: GHVU
Center clone name: CH230-92M16
----- Summary Statistics
Assembly program: Phrap; version 0.990329first call to findphraplist
Consensus quality: 65274 bases at least Q40
Consensus quality: 72009 bases at least Q30
Consensus quality: 78781 bases at least Q20
Estimated insert size: 56261; sum-of-contrigs estimation
Quality coverage: 0x in Q20 bases; agarose-rip estimation
Quality coverage: 0.6x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 52 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 3180: contrig of 3180 bp in length
3181 3280: gap of unknown length
3281 6404: contrig of 3124 bp in length
6405 6504: gap of unknown length
6505 8428: contrig of 1924 bp in length
8429 8528: gap of unknown length
8529 11087: contrig of 2559 bp in length
11088 11187: gap of unknown length
11188 13014: contrig of 1827 bp in length
13015 13114: gap of unknown length
13115 15465: contrig of 2351 bp in length
15466 17263: gap of unknown length
17264 17363: gap of unknown length
17364 20502: contrig of 3139 bp in length
20503 20602: gap of unknown length
20603 22851: contrig of 2249 bp in length
22852 22951: gap of unknown length
22952 24526: contrig of 1575 bp in length
24527 24626: gap of unknown length
24627 26619: contrig of 1993 bp in length
26620 28232: gap of unknown length
28233 28332: contrig of 1513 bp in length
28333 30047: gap of unknown length
30048 30147: gap of unknown length
30148 32351: contrig of 2204 bp in length
32352 32451: gap of unknown length
32452 34547: contrig of 2096 bp in length
34548 34647: gap of unknown length
34649 35680: contrig of 1033 bp in length
35681 35780: gap of unknown length
35781 37417: contrig of 1637 bp in length
37418 37517: gap of unknown length
37519 39065: contrig of 1548 bp in length
39066 39165: gap of unknown length
39166 40772: contrig of 1607 bp in length
40773 40872: gap of unknown length
40873 42964: contrig of 2092 bp in length
42965 43064: gap of unknown length
43065 44349: contrig of 1285 bp in length
44350 44449: gap of unknown length
44450 46087: contrig of 1638 bp in length
46088 46187: gap of unknown length
46188 47814: contrig of 1627 bp in length
47815 47914: gap of unknown length
47915 49269: contrig of 1355 bp in length

49270 49369: gap of unknown length
49370 50548: contrig of 1179 bp in length
50549 50648: gap of unknown length
50649 52335: contrig of 1687 bp in length
52336 52435: gap of unknown length
52436 53644: contrig of 1209 bp in length
53645 53744: gap of unknown length
53745 54804: contrig of 1060 bp in length
54805 54904: gap of unknown length
54905 56452: contrig of 1548 bp in length
56453 56552: gap of unknown length
56553 57929: contrig of 1377 bp in length
57930 58029: gap of unknown length
58030 59058: contrig of 1029 bp in length
59059 59158: gap of unknown length
59159 60586: contrig of 1428 bp in length
60587 60686: gap of unknown length
60687 62056: contrig of 1370 bp in length
62057 62156: gap of unknown length
62157 63583: contrig of 1427 bp in length
63584 63683: gap of unknown length
63684 65026: contrig of 1343 bp in length
65027 65127: gap of unknown length
65128 66522: contrig of 1396 bp in length
66523 67819: gap of unknown length
67820 67919: contrig of 1197 bp in length
67920 69078: gap of unknown length
69079 69178: contrig of 1159 bp in length
69179 70267: gap of unknown length
70268 70367: contrig of 1089 bp in length
70368 71457: gap of unknown length
71458 71557: gap of unknown length
71558 72569: contrig of 1012 bp in length
72569 72669: gap of unknown length
72670 74152: contrig of 1483 bp in length
74153 74252: gap of unknown length
74253 75490: contrig of 1238 bp in length
75491 75590: gap of unknown length
75591 76595: contrig of 1005 bp in length
76596 76695: gap of unknown length
76696 78165: contrig of 1470 bp in length
78166 78265: gap of unknown length
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79582 80743: contrig of 1162 bp in length
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80844 81859: contrig of 1016 bp in length
81860 81959: gap of unknown length
81960 83220: contrig of 1261 bp in length
83221 83320: gap of unknown length
83321 84499: contrig of 1179 bp in length
84499 84599: gap of unknown length
84600 86124: contrig of 1525 bp in length
86125 86224: gap of unknown length
86225 87421: contrig of 1197 bp in length.

FEATURES
source
1. 87421
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-92M16"

BASE COUNT 21196 a 20644 c 20168 g 20216 t 5197 others
ORIGIN

Query Match 75.3%; Score 22.6; DB 2; Length 87421;
Best local Similarity 86.2%; Pred. No. 40;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ttggcagcagcaagtcgcgattgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 39795 TGGGCAACACCAAGTCGAAATGCAGGTAC 39767

LOCUS	BC008593	2004 bp	mRNA	linear	PRI 12-JUL-2001
DEFINITION	BC008593	Human sapiens, clone IMAGE:3458856, mRNA, partial cds.			
ACCESSION	BC008593				
VERSION	BC008593.1	GI:14250326			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2004)				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Strausberg, R.				
JOURNAL	Direct Submission				
	Submitted (23-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalona@bcm.tmc.edu Villalona, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.				
FEATURES	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>Series: IRAC Plate: 19 Row: j Column: 11.</p> <p>Location/Qualifiers</p> <p>1..2004</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:3458856"</p> <p>/tissue_type="Cervix, carcinoma"</p> <p>/clone_lib="NIH MGC_12"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pCMV-SPORT6"</p> <p><1..1560</p> <p>/codon_start=1</p> <p>/product="unknown (protein for IMAGE:3458856)"</p> <p>/protein_id="AAH08593.1"</p> <p>/db_xref="GI:14250327"</p> <p>/translation="VLRVSLVWLHYGGRDFGPHGHARTGLGSPSSPGRCSGPNR PONSVRQGGSGRQHVLMEITLSKVSFQHEVYVAEPATGAAASOLEEERPLSRQV IVOLLEVDRILASSQINKFLYLRHSEMRPRASHNMLTIKALHVAPTNLGGPECCAR VSLMLRLVNDQDALPFLKDFETSLVINGVETSAEARPETRAOPSSPLEGQABE GVETTPGSEAPVGGGSHSPDPQOPITVREFPFSEVPIWLDYHGKHVYMOVGFAGI LIGLAQINSEIKRKLCRRHGLGVGVKUYALNEMQLQDRKQJLGLGAGVPMHS VVOLEFGFRDLMLPIEQYRKDGRLMRGLGAGASFSSTASALEVSNLVQATQAT AEVYTDILSPAPVSRSLQDRKRLRRRRCQPPADLEGVAKADVIREGLIDTAQITII CDVASRHEQKGLGAGVGIROLPPYIVVPLIATATSSILGGMNNOIYPDANKDH ALKRRSDSAD"</p>				
CDS	<p>360 a 679 c 613 g 352 t</p>				
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ORIGIN					
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Best Local Similarity	85.2%	Pred. No. 3e+02;			
Matches 23;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;	
4 ggcagcaccagtcgcgattgcagatcc 30					
170 gccacgaccatgctctcatggagatcc 196					

[illegible]

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LPIEYRKDGRLMRJLGGASFGSSSTALET.SNRLOAOLQATAEYDILSPAP
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TGAVGGVIRLPPTVYKLLIATEXTSSILGSMRQIYPDANKDHALMKRSDSAD"

BASE COUNT 1124 a 2128 c 1897 g 1150 t

ORIGIN

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Best Local Similarity 85.2%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcagcaatcaatccgagtcgagatcc 30
|||||
DB 4483 GGCAGCATCATGCTCCCATGAGATCC 4509

RESULT 25
AC084075/c
LOCUS
DEFINITION AC084075 61633 bp DNA linear HNG 12-OCT-2000
Homo sapiens chromosome 11 clone CTD-2380K20 map 11, LOW-PASS
SEQUENCE SAMPLING.
AC084075
VERSION AC084075.1 GI:10799439
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 61633)
JOURNAL Birren,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE Homo sapiens chromosome 11, clone CTD-2380K20
AUTHORS Unpublished
2 (bases 1 to 61633)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
Bouckegalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chapel,Y., Colangelo,M., Collins,A., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRoque,K.,
Llamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marcus,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrum,J., Menus,L., Mihova,T., Mienga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisan,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rodov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Saugner,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,U., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.

Direct Submission
Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: I10806
Center clone name: 2380_K_20

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be generic and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 663: contig of 663 bp in length
664 763: gap of 100 bp
764 1437: contig of 674 bp in length
1438 1537: gap of 100 bp
1538 2244: contig of 707 bp in length
2245 2344: gap of 100 bp
2345 3028: contig of 684 bp in length
3029 3128: gap of 100 bp
3129 3803: contig of 675 bp in length
3804 3903: gap of 100 bp
3904 4582: contig of 679 bp in length
4583 4682: gap of 100 bp
4683 5371: contig of 689 bp in length
5372 5471: gap of 100 bp
5472 6140: contig of 669 bp in length
6141 6240: gap of 100 bp
6241 6914: contig of 674 bp in length
6915 7014: gap of 100 bp
7015 7686: contig of 672 bp in length
7687 7786: gap of 100 bp
7787 8477: contig of 691 bp in length
8478 8577: gap of 100 bp
8578 9276: contig of 699 bp in length
9277 9376: gap of 100 bp
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10047 10146: gap of 100 bp
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10836 10935: gap of 100 bp
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13249 13915: contig of 667 bp in length
13916 14015: gap of 100 bp
14016 14693: contig of 678 bp in length
14694 14793: gap of 100 bp
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15465 15564: gap of 100 bp
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17915 18594: contig of 680 bp in length
18595 18694: gap of 100 bp
18695 19371: contig of 677 bp in length
19372 19471: gap of 100 bp
19472 20135: contig of 664 bp in length
20136 20235: gap of 100 bp
20236 20913: contig of 678 bp in length
20914 21013: gap of 100 bp
21014 21661: contig of 648 bp in length
21662 21761: gap of 100 bp
21762 22438: contig of 677 bp in length
22439 22538: gap of 100 bp
22539 23244: contig of 706 bp in length
23245 23344: gap of 100 bp
23345 24006: contig of 662 bp in length
24007 24106: gap of 100 bp
24107 24800: contig of 694 bp in length
24801 24900: gap of 100 bp
24901 25593: contig of 693 bp in length
25594 25693: gap of 100 bp

25694 26386: contig of 693 bp in length
 * 26387 26486: gap of 100 bp
 * 26487 27136: contig of 650 bp in length
 * 27137 27236: gap of 100 bp
 * 27237 27934: contig of 698 bp in length
 * 27935 28034: gap of 100 bp
 * 28035 28709: contig of 675 bp in length
 * 28710 28809: gap of 100 bp
 * 28810 29480: contig of 671 bp in length
 * 29481 29580: gap of 100 bp
 * 29581 30252: contig of 672 bp in length
 * 30253 30352: gap of 100 bp
 * 30353 31017: contig of 665 bp in length
 * 31018 31117: gap of 100 bp
 * 31118 31852: contig of 735 bp in length
 * 31853 31952: gap of 100 bp
 * 31953 32642: contig of 690 bp in length
 * 32643 32742: gap of 100 bp
 * 32743 33439: contig of 697 bp in length
 * 33440 33539: gap of 100 bp
 * 33540 34229: contig of 690 bp in length
 * 34230 34329: gap of 100 bp
 * 34330 35029: contig of 700 bp in length
 * 35030 35129: gap of 100 bp
 * 35130 35825: contig of 696 bp in length
 * 35826 35925: gap of 100 bp
 * 35926 36606: contig of 681 bp in length
 * 36607 36706: gap of 100 bp
 * 36707 37362: contig of 656 bp in length
 * 37363 37462: gap of 100 bp
 * 37463 38129: contig of 667 bp in length
 * 38130 38229: gap of 100 bp
 * 38230 38903: contig of 674 bp in length
 * 38904 39003: gap of 100 bp
 * 39004 39681: contig of 678 bp in length
 * 39682 39781: gap of 100 bp
 * 39782 40469: contig of 688 bp in length
 * 40470 40569: gap of 100 bp
 * 40570 41258: contig of 689 bp in length
 * 41259 41358: gap of 100 bp
 * 41359 42053: contig of 695 bp in length
 * 42054 42153: gap of 100 bp
 * 42154 42805: contig of 652 bp in length
 * 42806 42905: gap of 100 bp
 * 42906 43559: contig of 654 bp in length
 * 43560 43659: gap of 100 bp
 * 43660 44324: contig of 665 bp in length
 * 44325 44424: gap of 100 bp
 * 44425 45087: contig of 663 bp in length
 * 45088 45187: gap of 100 bp
 * 45188 45878: contig of 691 bp in length
 * 45879 45978: gap of 100 bp
 * 45979 46645: contig of 667 bp in length
 * 46646 46745: gap of 100 bp
 * 46746 47439: contig of 694 bp in length
 * 47440 47539: gap of 100 bp
 * 47540 48230: contig of 691 bp in length
 * 48231 48330: gap of 100 bp
 * 48331 49027: contig of 697 bp in length
 * 49028 49127: gap of 100 bp
 * 49128 49798: contig of 671 bp in length
 * 49799 49898: gap of 100 bp
 * 49899 50566: contig of 668 bp in length
 * 50567 50666: gap of 100 bp
 * 50667 51354: contig of 688 bp in length
 * 51355 51454: gap of 100 bp
 * 51455 52137: contig of 683 bp in length
 * 52138 52237: gap of 100 bp
 * 52238 52905: contig of 668 bp in length
 * 52906 53005: gap of 100 bp
 * 53006 53685: contig of 680 bp in length
 * 53686 53785: gap of 100 bp
 * 53786 54487: contig of 702 bp in length

Query Match 68.7%: Score 20.6; DB 2; Length 61633;
 Best Local Similarity 85.2%: Pred. No. 2.9e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 ggcagacccaagtcgcgatcc 30
 Db 12760 GGCAGACCATGCTCCTCATGAGATCC 12734
 ||||||| ||||| ||| |||||

RESULT 26

AC000159 108523 bp DNA linear PRI 04-APR-2001
 LOCUS Homo sapiens Chromosome 11q13 BAC Clone b79g17, complete sequence.
 DEFINITION AC000159
 AC000159
 VERSION AC000159.6 GI:4417315
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Emmert-Buck,M.R., Debelenko,L.V., Zhuang,Z., Lubensky,I.A. and Liotta,L.A.
 TITLE Sequence of a 11q13 bac mapping distal to PYGM and proximal to D11S4936
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 108523)
 AUTHORS Weisemann,J. and Boguski,M.S.
 TITLE Sequence of a 11q13 bac mapping distal to PYGM and proximal to D11S4936

JOURNAL

AUTHORS Agarwal,S.K., Kester,M., Kim,Y.S., Heppner,C., Dong,Q., Spiegel,A.M., Burns,L.A. and Marx,S.J.
 TITLE Sequence of a 11q13 bac mapping distal to PYGM and proximal to D11S4936
 JOURNAL Unpublished

REFERENCE

AUTHORS Chandrasekharappa,S.C., Guru,S.C., Manickam,P., Olufole,S.-E. and Collins,F.S.
 TITLE Unpublished
 JOURNAL 4 (bases 1 to 108523)
 AUTHORS Wang,Y. and Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAR-1997) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE

AUTHORS Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE

AUTHORS Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE

AUTHORS Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE

AUTHORS Fu,Y., Pan,H., Wang,Y., Dorman,A.F., Dolance,J.E., Smith,B.T., Meadows,S.M. and Roe,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 10 (bases 1 to 108523)
AUTHORS Fu, Y., Pan, H., Wang, Y., Dorman, A.F., Dolance, J.E., Smith, B.T.,
Meadows, S.M. and Roe, B.A.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Mar 16, 1999 this sequence version replaced gi:438739.
FEATURES
 Source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="11"
 /chrosome="11q13"
 /map="11q13"
 /clone="b79g17"
BASE COUNT 24680 a 28863 c 28496 g 26484 t
ORIGIN

Query Match 68.7%; Score 20.6; DB 9; Length 108523;
Best Local Similarity 85.2%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 4 gccagcaccacgaagtcgcgagtcagatcc 30
 ||||| 1111 111 1111111
Db 72176 GGCACGACCACATGCTCCTCATGGAGATCC 72202

RESULT 27
LOCUS AP000814 135337 bp DNA linear HTG 31-MAY-2000
DEFINITION Homo sapiens chromosome 11 clone XXPac-969D11 map 11q13, WORKING
DRAFT SEQUENCE, 31 unordered pieces.
ACCESSION AP000814
VERSION AP000814.2 GI:81331587
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone:XXPac-969D11.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 135237)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 135,237 genomic DNA of 11q13
Published Only in Database (1999) In press
2 (bases 1 to 135237)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (30-NOV-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitaaso Univ., 1-15-1 Kitaaso, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hnp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997651.
COMMENT
 Genome Center
 Center: RIKEN Genomic Sciences Center(GSC)
 Web site: http://hnp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 Project Information
 Center project name: Humrap11
 Center clone name: XXPac-969D11
 Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 116075 bases at least 40
 Consensus quality: 124675 bases at least 30
 Consensus quality: 129566 bases at least 20
 Insert size: 132237; sum-of-contrigs

```

Quality coverage: 4.10x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
31 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

1      14762 contig of 14762 bp in length
14863      22747 contig of 7885 bp in length
22848      31877 contig of 9030 bp in length
31878      40788 contig of 8811 bp in length
40889      50262 contig of 9374 bp in length
50363      56310 contig of 5348 bp in length
56411      61057 contig of 4647 bp in length
61158      68219 contig of 7062 bp in length
68320      74590 contig of 6271 bp in length
74691      79328 contig of 4638 bp in length
79429      83930 contig of 4502 bp in length
84031      88711 contig of 4681 bp in length
88812      93107 contig of 4172 bp in length
93107      97278 contig of 4172 bp in length
97278      101644 contig of 4666 bp in length
101644      103787 contig of 2043 bp in length
103787      106271 contig of 2284 bp in length
106372      110210 contig of 3839 bp in length
110311      112278 contig of 1968 bp in length
112379      114714 contig of 2336 bp in length
114815      117772 contig of 2958 bp in length
117873      120347 contig of 2475 bp in length
120448      121697 contig of 1250 bp in length
121798      123307 contig of 2110 bp in length
124008      125646 contig of 1639 bp in length
125747      127154 contig of 1408 bp in length
127255      129449 contig of 2195 bp in length
129550      130823 contig of 1274 bp in length
130924      132904 contig of 1981 bp in length
133005      134058 contig of 1054 bp in length
134159      135237 contig of 1079 bp in length

Sequence updated (26-May-2000).
NOTE: This is a 'working draft' sequence. It currently
consists of 31 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of 'N', but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1      14762: contig of 14762 bp in length
14763      14862: gap of 100 bp
14863      22747: contig of 7885 bp in length
22748      22847: gap of 100 bp
22848      31877: contig of 9030 bp in length
31878      31977: gap of 100 bp
31978      40788: contig of 8811 bp in length
40789      40888: gap of 100 bp
40889      50262: contig of 9374 bp in length
50263      50362: gap of 100 bp
50363      56310: contig of 5348 bp in length
56311      56410: gap of 100 bp
56411      61057: contig of 4647 bp in length
61058      61157: gap of 100 bp
61158      68219: contig of 7062 bp in length
68220      68319: gap of 100 bp
68320      74590: contig of 6271 bp in length
74591      74690: gap of 100 bp
74691      79328: contig of 4638 bp in length
79329      79428: gap of 100 bp
79429      83930: contig of 4502 bp in length
83931      84030: gap of 100 bp
84031      88711: contig of 4681 bp in length
88712      88811: gap of 100 bp

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```

* 88812 93006: contig of 4195 bp in length
* 93007 93106: gap of 100 bp
* 93107 97278: contig of 4172 bp in length
* 97279 97378: gap of 100 bp
* 97379 101644: contig of 4266 bp in length
* 101645 101744: gap of 100 bp
* 101745 103787: contig of 2043 bp in length
* 103788 103887: gap of 100 bp
* 103888 106271: contig of 2384 bp in length
* 106272 106371: gap of 100 bp
* 106372 110210: contig of 3839 bp in length
* 110211 110310: gap of 100 bp
* 110311 112278: contig of 1968 bp in length
* 112279 112787: gap of 100 bp
* 112788 114714: contig of 2336 bp in length
* 114715 114814: gap of 100 bp
* 114815 117772: contig of 2958 bp in length
* 117773 117872: gap of 100 bp
* 117873 120347: contig of 2475 bp in length
* 120348 120447: gap of 100 bp
* 120448 121697: contig of 1250 bp in length
* 121698 121797: gap of 100 bp
* 121798 123907: contig of 2110 bp in length
* 123908 124007: gap of 100 bp
* 124008 125646: contig of 1639 bp in length
* 125647 125746: gap of 100 bp
* 125747 127154: contig of 1408 bp in length
* 127155 127254: gap of 100 bp
* 127255 129449: contig of 2195 bp in length
* 129450 129549: gap of 100 bp
* 129550 130823: contig of 1274 bp in length
* 130824 130923: gap of 100 bp
* 130924 132904: contig of 1981 bp in length
* 132905 133004: gap of 100 bp
* 133005 134058: contig of 1054 bp in length
* 134059 134158: gap of 100 bp
* 134159 135237: contig of 1079 bp in length.

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FEATURES

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source
1. 135237
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   /db_xref="taxon:9606"
   /chromosome="11"
   /map="11q13"
   /clone="Xpacc-969D11"
misc_feature
1. 14762
   /note="assembly_fragment"
misc_feature
14863..22747
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misc_feature
22848..31877
   /note="assembly_fragment"
misc_feature
31978..40788
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Query Match      68.7%  Score 20.6; DB 2; Length 135237;
Best Local Similarity 85.2%  Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

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Oy 4 ggcagcaccacagtcgcagatcgatcc 30
||||| 111111111111111111111111
Db 119819 GCGAGCACCATGTCTCATGAGATCC 119845

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```

RESULT 28
AP001187/c 166269 bp DNA linear HTG 17-JAN-2001
LOCUS Homo sapiens chromosome 11 clone RP11-665N17 map 11q13, WORKING
DEFINITION DRAFT SEQUENCE, 27 unordered pieces.
ACCESSION AP001187.3 GI:12245852
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens DNA, clone:RP11-665N17.
SOURCE Homo sapiens
ORGANISM Homo sapiens

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REFERENCE
1 (bases 1 to 166269)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 166,269 genomic DNA of 11q13
Published Only in Database (2000) In press
2 (bases 1 to 166269)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (18-FEB-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jan 16, 2001 this sequence version replaced gi:8117633.

```

```

JOURNAL
TITLE
JOURNAL
AUTHORS
REFERENCE
AUTHORS
COMMENT

```

```

Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information -----
Center project name: HumDrafi11
Center clone name: RP11-665N17
----- Summary Statistics -----
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 156782 bases at least Q40
Consensus quality: 160361 bases at least Q30
Consensus quality: 162264 bases at least Q20
Insert size: 163669; sum-of-contigs
Quality coverage: 8.32x in Q20 bases; sum-of-contigs

```

NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be

```
preserved
1 28395 contig of 28395 bp in length
28496 43446 contig of 14951 bp in length
43547 58083 contig of 14537 bp in length
58184 66868 contig of 8685 bp in length
66969 76574 contig of 9606 bp in length
76675 86418 contig of 9744 bp in length
86519 94044 contig of 7526 bp in length
94145 100790 contig of 6646 bp in length
100891 108539 contig of 7649 bp in length
108640 115961 contig of 7322 bp in length
116062 120258 contig of 4197 bp in length
120359 125359 contig of 5001 bp in length
125460 130186 contig of 4727 bp in length
130287 134400 contig of 4114 bp in length
134501 139064 contig of 4564 bp in length
139065 143906 contig of 4742 bp in length
143907 148280 contig of 4274 bp in length
148281 151006 contig of 2626 bp in length
151007 153748 contig of 2642 bp in length

NOTE: This is a 'working draft' sequence. It currently
consists of 27 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 28395: contig of 28395 bp in length
28396 28495: gap of 100 bp
28496 43446: contig of 14951 bp in length
43447 43546: gap of 100 bp
43547 58083: contig of 14537 bp in length
58084 58183: gap of 100 bp
58184 66868: contig of 8685 bp in length
66869 66968: gap of 100 bp
66969 76574: contig of 9606 bp in length
76575 76674: gap of 100 bp
76675 86418: contig of 9744 bp in length
86419 86518: gap of 100 bp
86519 94044: contig of 7526 bp in length
94045 94144: gap of 100 bp
94145 100790: contig of 6646 bp in length
100791 100890: gap of 100 bp
100891 108539: contig of 7649 bp in length
108540 108639: gap of 100 bp
108640 115961: contig of 7322 bp in length
115962 116061: gap of 100 bp
116062 120258: contig of 4197 bp in length
120259 120358: gap of 100 bp
120359 125359: contig of 5001 bp in length
125360 125459: gap of 100 bp
125460 130186: contig of 4727 bp in length
130187 130286: gap of 100 bp
130287 134400: contig of 4114 bp in length
134401 134500: gap of 100 bp
134501 139064: contig of 4564 bp in length
139065 139164: gap of 100 bp
139165 143906: contig of 4742 bp in length
143907 144006: gap of 100 bp
144007 148280: contig of 4274 bp in length
148281 148380: gap of 100 bp
148381 151006: contig of 2626 bp in length
151007 151106: gap of 100 bp
151107 153748: contig of 2642 bp in length
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FEATURES
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* 153849 155555: contig of 1707 bp in length
* 155556 155655: gap of 100 bp
* 155656 157198: contig of 1543 bp in length
* 157199 157298: gap of 100 bp
* 157299 159872: contig of 2574 bp in length
* 159873 159972: gap of 100 bp
* 159973 161499: contig of 1527 bp in length
* 161500 161599: gap of 100 bp
* 161600 162703: contig of 1104 bp in length
* 162704 162803: gap of 100 bp
* 162804 163847: contig of 1044 bp in length
* 163848 163947: gap of 100 bp
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* 165122 165221: gap of 100 bp
* 165222 166269: contig of 1048 bp in length.
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/map="11q13"
/clone="RP11-665N17"
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/feature="assembly_fragment"
43547.58083
/feature="assembly_fragment"
58184.66868
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/feature="assembly_fragment"
76675.86418
/feature="assembly_fragment"
86519.94044
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94145.100790
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100891.108539
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116062.120258
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120359.125359
/feature="assembly_fragment"
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134501.139064
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157299.159872
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159973.161499
/feature="assembly_fragment"
161600.162703
/feature="assembly_fragment"
162804.163847
/feature="assembly_fragment"
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misc-feature 165222. .166269 /note="assembly-fragment"
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Query Match 68.7%; Score 20.6; DB 2; Length 166269;
Best Local Similarity 85.2%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 ggcagcaccagtcgcgagcagatcc 30
Db 56114 GGCAGCACCATGCTCATGAGATCC 56088
RESULT 29
AP000928/c
LOCUS AP000928 171980 bp DNA linear HMG 30-MAY-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-772K10 map 11q13, WORKING
DRAFT SEQUENCE, 33 unordered pieces.
ACCESSION AP000928
VERSION AP000928.2 GI:8119069
KEYWORDS HTG; HMGs_PHASE1; HMGs_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-772K10.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 171,980 genomic DNA of 11q13
2 (bases 1 to 171980)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitsano Univ., 1-15-1 Kitsato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997744.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humdrift11
Center clone name: RP11-772K10
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 14109 bases at least Q40
Consensus quality: 154862 bases at least Q30
Consensus quality: 163556 bases at least Q20
Insert size: 166780; sum-of-contigs
Quality coverage: 3.98x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
33 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 13598 contig of 13598 bp in length
13699 26815 contig of 13117 bp in length
26916 37862 contig of 10947 bp in length
37963 46388 contig of 8426 bp in length
46489 55060 contig of 8572 bp in length

55161 61498 contig of 6338 bp in length
61599 68961 contig of 7263 bp in length
69062 76351 contig of 7392 bp in length
76454 84390 contig of 7937 bp in length
84491 91104 contig of 6614 bp in length
91205 97347 contig of 6143 bp in length
97448 103810 contig of 6563 bp in length
103911 110422 contig of 6512 bp in length
110523 116801 contig of 6279 bp in length
116902 121989 contig of 5088 bp in length
122090 125946 contig of 3857 bp in length
126047 132109 contig of 6063 bp in length
132210 136422 contig of 4213 bp in length
136522 140566 contig of 4044 bp in length
140667 144574 contig of 3908 bp in length
144675 148311 contig of 3637 bp in length
148412 150652 contig of 2241 bp in length
150753 153335 contig of 2583 bp in length
153436 155668 contig of 2233 bp in length
155769 158851 contig of 3083 bp in length
158952 161241 contig of 2290 bp in length
161342 163307 contig of 1966 bp in length
163408 165487 contig of 2080 bp in length
165588 167734 contig of 2147 bp in length
167835 168855 contig of 1021 bp in length
168956 170089 contig of 1134 bp in length
170190 170655 contig of 466 bp in length
170756 171980 contig of 1225 bp in length
Sequence updated (26-May-2000)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 13598: contig of 13598 bp in length
* 13599 13698: gap of 100 bp
* 13699 26815: contig of 13117 bp in length
* 26816 26915: gap of 100 bp
* 26916 37862: contig of 10947 bp in length
* 37863 37962: gap of 100 bp
* 37963 46388: contig of 8426 bp in length
* 46389 46488: gap of 100 bp
* 46489 55060: contig of 8572 bp in length
* 55061 55160: gap of 100 bp
* 55161 61498: contig of 6338 bp in length
* 61499 61598: gap of 100 bp
* 61599 68961: contig of 7363 bp in length
* 68962 69061: gap of 100 bp
* 69062 76351: contig of 7292 bp in length
* 76352 76453: gap of 100 bp
* 76454 84390: contig of 7937 bp in length
* 84391 84490: gap of 100 bp
* 84491 91104: contig of 6614 bp in length
* 91105 91204: gap of 100 bp
* 91205 97347: contig of 6143 bp in length
* 97348 97447: gap of 100 bp
* 97448 103810: contig of 6563 bp in length
* 103811 103910: gap of 100 bp
* 103911 110422: contig of 6512 bp in length
* 110423 110522: gap of 100 bp
* 110523 116801: contig of 6279 bp in length
* 116802 116901: gap of 100 bp
* 116902 121989: contig of 5088 bp in length
* 121990 122089: gap of 100 bp
* 122090 125946: contig of 3857 bp in length
* 125947 126046: gap of 100 bp
* 126047 132109: contig of 6063 bp in length
* 132110 132209: gap of 100 bp
* 132210 136422: contig of 4213 bp in length
* 136423 136522: gap of 100 bp

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* 136523 140566: contig of 4044 bp in length
* 140567 140566: gap of 100 bp in length
* 140667 144574: contig of 3908 bp in length
* 144575 144674: gap of 100 bp in length
* 144675 148311: contig of 3637 bp in length
* 148312 148411: gap of 100 bp in length
* 148412 150652: contig of 2241 bp in length
* 150653 150752: gap of 100 bp in length
* 150753 153335: contig of 2583 bp in length
* 153336 153435: gap of 100 bp in length
* 153436 155668: contig of 2233 bp in length
* 155669 155768: gap of 100 bp in length
* 155769 158851: contig of 3083 bp in length
* 158852 158951: gap of 100 bp in length
* 158952 161241: contig of 2290 bp in length
* 161242 161341: gap of 100 bp in length
* 161342 163307: contig of 1966 bp in length
* 163308 163407: gap of 100 bp in length
* 163408 165487: contig of 2080 bp in length
* 165488 165587: gap of 100 bp in length
* 165588 167734: contig of 2147 bp in length
* 167735 167834: gap of 100 bp in length
* 167835 168855: contig of 1021 bp in length
* 168856 168955: gap of 100 bp in length
* 168956 170089: contig of 1134 bp in length
* 170090 170189: gap of 100 bp in length
* 170190 170655: contig of 466 bp in length
* 170656 170755: gap of 100 bp in length
* 170756 171980: contig of 1225 bp in length.

FEATURES
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1. 171980
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/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/clone="RP11-772K10"
1. 13598
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misc_feature 13699..26815
/note="assembly-fragment"
misc_feature 26916..37862
/note="assembly-fragment"
misc_feature 37963..46388
/note="assembly-fragment clone_end:SP6 vector_side:right"
misc_feature 46489..55060
/note="assembly-fragment"
misc_feature 55161..61498
/note="assembly-fragment"
misc_feature 61599..68961
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misc_feature 69062..76353
/note="assembly-fragment"
misc_feature 76454..84390
/note="assembly-fragment"
misc_feature 84491..91104
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misc_feature 91205..97347
/note="assembly-fragment"
misc_feature 97448..103810
/note="assembly-fragment"
misc_feature 103911..110422
/note="assembly-fragment"
misc_feature 110523..116801
/note="assembly-fragment"
misc_feature 116902..121989
/note="assembly-fragment"
misc_feature 122090..125946
/note="assembly-fragment"
misc_feature 126047..132109
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misc_feature 132210..136422
/note="assembly-fragment"

Query Match 68.7%; Score 20.6; DB 2; Length 171980;

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Best Local Similarity 85.2%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcagaccacgaagtcgcagatcgatcc 30
|||||  |||  |||  |||  |||
Db 25058 GGCAGACCATGCTCATGAGATCC 25032

RESULT 30
AP001558
LOCUS
DEFINITION
Homo sapiens chromosome 11 clone RP11-686D5 map 11q13, WORKING
DRAFT SEQUENCE, 40 unordered pieces.
ACCESSION
AP001558.2 GI:8117392
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Homo sapiens DNA, clone:RP11-686D5.
SOURCE
Homo sapiens
Organism
Eukaryota; Metazoa; Chordata; Carniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 178100)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 178,100 genomic DNA of 11q13
Published Only in Database (2000) In press
2 (bases 1 to 178100)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitsato Univ., 1-15-1 Kitsato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7380893.

----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraff11
Center clone name: RP11-686D5
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 148042 bases at least Q40
Consensus quality: 162125 bases at least Q30
Consensus quality: 169512 bases at least Q20
Insert size: 174200; sum-of-contigs
Quality coverage: 4.12x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
40 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 20070 contig of 20070 bp in length
1 20171 34749 contig of 14579 bp in length
34850 50049 contig of 15200 bp in length
50150 60765 contig of 10616 bp in length
60866 67727 contig of 6862 bp in length
67828 76362 contig of 8535 bp in length
76463 82230 contig of 5765 bp in length
82331 89521 contig of 7191 bp in length
89622 95129 contig of 5508 bp in length
95230 101095 contig of 5866 bp in length
101196 106255 contig of 5060 bp in length
106356 110801 contig of 4446 bp in length

```

110902 114837 contig of 3936 bp in length
114938 120430 contig of 5493 bp in length
120531 125238 contig of 4708 bp in length
125339 128370 contig of 3032 bp in length
128471 131184 contig of 2714 bp in length
131285 134627 contig of 3343 bp in length
134728 137446 contig of 2719 bp in length
137547 140281 contig of 2735 bp in length
140382 142601 contig of 2220 bp in length
142702 145477 contig of 2776 bp in length
145578 148565 contig of 2988 bp in length
148666 151182 contig of 2517 bp in length
151283 153836 contig of 2534 bp in length
153937 156236 contig of 2300 bp in length
156337 157818 contig of 1482 bp in length
157919 159802 contig of 1884 bp in length
159903 161284 contig of 1382 bp in length
161385 163110 contig of 1726 bp in length
163211 164636 contig of 1426 bp in length
164737 166593 contig of 1857 bp in length
166694 167867 contig of 1174 bp in length
167968 169543 contig of 1576 bp in length
169644 170824 contig of 1181 bp in length
170925 172804 contig of 1880 bp in length
172905 173997 contig of 1093 bp in length
174098 175750 contig of 1653 bp in length
175851 176984 contig of 1134 bp in length
177085 178100 contig of 1016 bp in length

Sequence updated (26-May-2006).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 20070: contig of 20070 bp in length
20071 20170: gap of 100 bp
20171 34749: contig of 14579 bp in length
34750 34849: gap of 100 bp
34850 50049: contig of 15200 bp in length
50050 50149: gap of 100 bp
50150 60765: contig of 10616 bp in length
60766 60865: gap of 100 bp
60866 67727: contig of 6862 bp in length
67728 67827: gap of 100 bp
67828 76362: contig of 8535 bp in length
76363 76462: gap of 100 bp
76463 82230: contig of 5768 bp in length
82231 82330: gap of 100 bp
82331 89521: contig of 7191 bp in length
89522 89621: gap of 100 bp
89622 95129: contig of 5508 bp in length
95130 95229: gap of 100 bp
95230 101095: contig of 5866 bp in length
101096 101195: gap of 100 bp
101196 106255: contig of 5060 bp in length
106256 106355: gap of 100 bp
106356 110801: contig of 4446 bp in length
110802 110901: gap of 100 bp
110902 114837: contig of 3936 bp in length
114838 114937: gap of 100 bp
114938 120430: contig of 5493 bp in length
120431 120530: gap of 100 bp
120531 125238: contig of 4708 bp in length
125239 125338: gap of 100 bp
125339 128370: contig of 3032 bp in length
128371 128470: gap of 100 bp
128471 131184: contig of 2714 bp in length
131185 131284: gap of 100 bp
131285 134627: contig of 3343 bp in length
134628 134727: gap of 100 bp

* 134728 137446: contig of 2719 bp in length
* 137447 137546: gap of 100 bp
* 137547 140281: contig of 2735 bp in length
* 140282 140381: gap of 100 bp
* 140382 142601: contig of 2220 bp in length
* 142602 142701: gap of 100 bp
* 142702 145477: contig of 2776 bp in length
* 145478 145577: gap of 100 bp
* 145578 148565: contig of 2988 bp in length
* 148566 148665: gap of 100 bp
* 148666 151182: contig of 2517 bp in length
* 151183 151282: gap of 100 bp
* 151283 153836: contig of 2534 bp in length
* 153837 153936: gap of 100 bp
* 153937 156236: contig of 2300 bp in length
* 156237 156336: gap of 100 bp
* 156337 157818: contig of 1482 bp in length
* 157819 157918: gap of 100 bp
* 157919 159802: contig of 1884 bp in length
* 159803 159902: gap of 100 bp
* 159803 161284: contig of 1382 bp in length
* 161285 161384: gap of 100 bp
* 161385 163110: contig of 1726 bp in length
* 163111 163210: gap of 100 bp
* 163211 164636: contig of 1426 bp in length
* 164637 164736: gap of 100 bp
* 164737 166593: contig of 1857 bp in length
* 166594 166693: gap of 100 bp
* 166694 167867: contig of 1174 bp in length
* 167868 167967: gap of 100 bp
* 167968 169543: contig of 1576 bp in length
* 169544 169643: gap of 100 bp
* 169644 170824: contig of 1181 bp in length
* 170825 170924: gap of 100 bp
* 170925 172804: contig of 1880 bp in length
* 172805 172904: gap of 100 bp
* 172905 173997: contig of 1093 bp in length
* 173998 174097: gap of 100 bp
* 174098 175750: contig of 1653 bp in length
* 175751 175850: gap of 100 bp
* 175851 176984: contig of 1134 bp in length
* 176985 177084: gap of 100 bp
* 177085 178100: contig of 1016 bp in length.

FEATURES
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1. 178100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/clone="RP11-686D5"
1. 20070
/note="assembly_fragment"
20171. 34749
/note="assembly_fragment"
34850. 50049
/note="assembly_fragment"
50150. 60765
/note="assembly_fragment"
60866. 67727
/note="assembly_fragment"
67828. 76362
/note="assembly_fragment clone_end:SP6 vector_side:right"
76463. 82230
/note="assembly_fragment"

misc_feature
/note="assembly_fragment"
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Query Match 68.7%; Score 20.6; DB 2; Length 178100;
Best Local Similarity 85.2%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ggcagcaccaagtcgagatcgatcc 30
|||||
Db 155737 GGCAGCACATGTCATCGAGATCC 155763

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RESULT 31
AC090316 187483 bp DNA linear HTG 21-JUL-2001
LOCUS Homo sapiens chromosome 11 clone RP11-772K10 map 11, WORKING DRAFT
DEFINITION
SEQUENCE, 23 unordered pieces.
AC090316
AC090316.2 GT:14971266
AC090316.2 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 187483)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Homo sapiens chromosome 11, clone RP11-772K10
REFERENCE 2 (bases 1 to 187483)
AUTHORS Unpublished
Bairren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collumore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRoque,K., Lamazares,R., Landers,T.,
Lehoczky,J., Levine,R., Liu,G., Maclean,C., MacDonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Menes,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhng,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sounez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Struss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zemek,L., Zimmer,A. and Zody,W.
Direct Submission
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996:1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12585
Center clone name: 772.K.10
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 177293 bases at least Q40
Consensus quality: 181933 bases at least Q30
Consensus quality: 183738 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 185283; sum-of-ctnigs
Quality coverage: 6.3 in Q20 bases;
Quality coverage: 6.2 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

```

```

* be preserved.
1 9134: contig of 9134 bp in length
* 9135 9234: gap of 100 bp
* 9235 10076: contig of 842 bp in length
* 10077 10176: gap of 100 bp
* 10177 11210: contig of 1034 bp in length
* 11211 11310: gap of 100 bp
* 11311 11521: contig of 211 bp in length
* 11522 11621: gap of 100 bp
* 11622 13944: contig of 2323 bp in length
* 13945 14044: gap of 100 bp
* 14045 16117: contig of 2073 bp in length
* 16118 16217: gap of 100 bp
* 16218 35961: contig of 19744 bp in length
* 35962 36061: gap of 100 bp
* 36062 38758: contig of 2697 bp in length
* 38759 38858: gap of 100 bp
* 38859 42149: contig of 3291 bp in length
* 42150 42249: gap of 100 bp
* 42250 46505: contig of 4256 bp in length
* 46506 46605: gap of 100 bp
* 46606 51462: contig of 4857 bp in length
* 51463 51562: gap of 100 bp
* 51563 57004: contig of 5442 bp in length
* 57005 57104: gap of 100 bp
* 57105 64258: contig of 7154 bp in length
* 64259 64358: gap of 100 bp
* 64359 69102: contig of 4744 bp in length
* 69103 69202: gap of 100 bp
* 69203 80578: contig of 11376 bp in length
* 80579 80678: gap of 100 bp
* 80679 91084: contig of 10406 bp in length
* 91085 91184: gap of 100 bp
* 91185 99902: contig of 8718 bp in length
* 99903 100002: gap of 100 bp
* 100003 114020: contig of 14018 bp in length
* 114021 114120: gap of 100 bp
* 114121 128914: contig of 14794 bp in length
* 128915 129014: gap of 100 bp
* 129015 140836: contig of 11822 bp in length
* 140837 140936: gap of 100 bp
* 140937 162541: contig of 21605 bp in length
* 162542 162641: gap of 100 bp
* 162642 185670: contig of 23029 bp in length
* 185671 185770: gap of 100 bp
* 185771 187483: contig of 1713 bp in length.
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/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-772K10"
/clone_lib="RPC1-11 Human Male BAC"
1. 9134
/note="assembly-fragment"
clone_end:SP6
vector_side:left"
9235. 10076
/note="assembly-fragment"
10177. 11210
/note="assembly-fragment"
11311. 11521
/note="assembly-fragment"
11622. 13944
/note="assembly-fragment"
14045. 16117
/note="assembly-fragment"
16218. 35961
/note="assembly-fragment"
36062. 38758
/note="assembly-fragment"
38859. 42149

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                  1..21293
                  /clone_lib="RPC1-11 Human Male BAC"
                  /note="assembly_fragment"
                  vector_side:"left"
misc_feature      21394..22583
                  /note="assembly_fragment"
misc_feature      22684..23723
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                  /note="assembly_fragment"
misc_feature      26081..67365
                  /note="assembly_fragment"
misc_feature      67466..70288
                  /note="assembly_fragment"
misc_feature      70389..81723
                  /note="assembly_fragment"
misc_feature      81824..93377
                  /note="assembly_fragment"
misc_feature      93478..125021
                  /note="assembly_fragment"
misc_feature      125122..156983
                  /note="assembly_fragment"
misc_feature      157084..198328
                  /note="assembly_fragment"
misc_feature      198429..200026
                  /note="assembly_fragment"
                  clone_end:"T7"
                  vector_side:"right"
BASE COUNT      45868 a 55290 c 53297 g 44469 t 1102 others
ORIGIN

```

```

Query Match      68.7%; Score 20.6; DB 2; Length 200026;
Best Local Similarity 85.2%; Pred. No.2.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      4 ggcagcaccgaagtcgcgagtcagatcc 30
        ||||||| ||| || |||||
Db 169453 GGCAGCACCATGTCATCGATCGATCC 169479

```

```

RESULT 33
AC004076      41322 bp DNA linear PRI 29-JAN-1998
LOCUS      Homo sapiens chromosome 19, cosmid R30217, complete sequence.
DEFINITION
AC004076      AC004076.1 GI:2822142
VERSION
KEYWORDS
SOURCE
ORGANISM      human.
                Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                1 (bases 1 to 41322)
REFERENCE
AUTHORS      Lamerdin,J.E., McCreedy,P.M., Skowronski,E., Adamson,A.W.,
                Burkhart-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stillwagen,S.,
                Georgescu,A., Avila,J., Liu,S., Bruce,R., Quan,G., Montgomery,M.,
                Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.O. and
                Carrano,A.V.
TITLE      Sequence analysis of a 500 kb ZNF gene family- containing human
                contig in 19q13.4
JOURNAL
REFERENCE      2 (bases 1 to 41322)
AUTHORS      Lamerdin,J.E.
TITLE      Direct Submission
JOURNAL
COMMENT      Submitted (29-JAN-1998) Joint Genome Institute, Lawrence Livermore
                National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
                Map and sequence oriented from centromere to q telomere.
                Cosmid R30217 overlaps cosmid R28253 to the left and F18750 to the
                right.

```

```

FEATURES
source
location/Qualifiers
1..41322
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.4 between D19S303 and ZNF134"
/clone="R30217"
/cell_line="5H12-B"
/clone_lib="L119NC032 R chromosome 19-specific cosmid"
/note="cosmid library constructed at LNL, from flow-sorted
chromosomes from hybrid 5H12-B, which carries chromosome
19 as its only human chromosome."
1..1431
/note="BLASTN similarity to AC003002 (80114..81544);
match: 1, score: 1.8e-294; database searched: nt; Human
DNA from overlapping chromosome 19-specific cosmids R29515
and R28253, genomic sequence, complete sequence [Homo
sapiens]"
complement(10..98)
/rpt_family="MSTC"
383..680
/rpt_family="AluSc"
complement(989..1286)
/note="YDS similarity to AA229025 nc50c11.s1 NCI CGAP_Pt3
Homo sapiens CDNA clone IMAGE:1011572. Score: 550
identity: 290/300 (96%)."
1281..1318
/rpt_family="POIX_A"
complement(1443..1755)
/rpt_family="AluSp"
1917..2204
/rpt_family="AluSx"
complement(2735..2777)
/rpt_family="(CA)n"
3566..3652
/rpt_family="FRAW/FAM"
3671..3719
/rpt_family="MER4D"
complement(3720..4019)
/rpt_family="AluSp"
4047..4324
/rpt_family="MER4D"
4960..5217
/note="YDS similarity to multiple ESTs:
(4960..5217) AA446441 zw60d10.r1 Soares total fetus Nb2HF8
9w Homo sapiens CDNA clone 774451 5' similar to contains
LTR3.t2 LTR3 repetitive element;
(1..259): 98% identity~(4962..5216) AA195132 zr34b08.r1
Soares NhMpu S1 Homo sapiens CDNA clone 665271 5' similar
to contains LTR3.b1 LTR3 repetitive element; (1..253): 99%
identity~(4962..5216) W03459 za06e09.r1 Soares melanocyte
2NDH8 Homo sapiens CDNA clone 291784 5' similar to
contains LTR3.b1 LTR3 repetitive element;(1..253); 96%
identity.
and others."
complement(5599..5875)
/rpt_family="LINE2"
complement(6952..6980)
/rpt_family="AT-rich"
7067..7364
/rpt_family="AluSg"
complement(7488..7593)
/rpt_family="MIR"
7718..8134
/rpt_family="LTR3"
complement(8649..9102)
/rpt_family="LINE2"
9114..9386
/rpt_family="AluO"
9573..9676
/note="Predicted exon, program: gfall2exons_human_1.3,
frame: 1, quality: excellent, score: 90.000"
10469..10758
repeat_region

```



```

* 124307 127520: contig of 3214 bp in length
* 127521 127620: gap of unknown length
* 127621 131710: contig of 4090 bp in length
* 131711 131810: gap of unknown length
* 131811 135916: contig of 4106 bp in length
* 135917 136016: gap of unknown length
* 136017 138794: contig of 2778 bp in length
* 138795 138894: gap of unknown length
* 138895 144037: contig of 5143 bp in length
* 144038 144137: gap of unknown length
* 144138 146347: contig of 2210 bp in length
* 146348 146447: gap of unknown length
* 146448 150379: contig of 3932 bp in length
* 150380 150479: gap of unknown length
* 150480 154510: contig of 4031 bp in length
* 154511 154610: gap of unknown length
* 154611 157925: contig of 3315 bp in length
* 157926 158025: gap of unknown length
* 158026 160712: contig of 2687 bp in length
* 160713 160812: gap of unknown length
* 160813 163479: contig of 2667 bp in length
* 163480 163579: gap of unknown length
* 163580 165744: contig of 2165 bp in length
* 165745 165844: gap of unknown length
* 165845 168563: contig of 2719 bp in length.

FEATURES
    source
        1. 168563
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="3p"
            /clone="RP11-474M18"

BASE COUNT  51285 a 30469 c 30057 g 54000 t 2752 others

ORIGIN
Query Match      67.3%: Score 20.2; DB 2; Length 168563;
Best Local Similarity 88.0%: Pred. No. 4.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 6 cagcaccagtcgcgatccagatcc 30
DB 114893 CAGCACCAATCACCATCGCATCC 114917

RESULT 36
AC023547 178415 bp DNA linear HTG 26-MAY-2000
LOCUS Homo sapiens chromosome 1 clone RP11-474M18 map 1, WORKING DRAFT
DEFINITION AC023547
AC023547
AC023547.3 GI:8076834
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 178415)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 1, clone RP11-474M18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178415)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukhgelter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreltra,P., Fitzhugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., Mcpheeters,R., Meldrum,J.,

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TITLE
JOURNAL
COMMENT
* 124307 127520: contig of 3214 bp in length
* 127521 127620: gap of unknown length
* 127621 131710: contig of 4090 bp in length
* 131711 131810: gap of unknown length
* 131811 135916: contig of 4106 bp in length
* 135917 136016: gap of unknown length
* 136017 138794: contig of 2778 bp in length
* 138795 138894: gap of unknown length
* 138895 144037: contig of 5143 bp in length
* 144038 144137: gap of unknown length
* 144138 146347: contig of 2210 bp in length
* 146348 146447: gap of unknown length
* 146448 150379: contig of 3932 bp in length
* 150380 150479: gap of unknown length
* 150480 154510: contig of 4031 bp in length
* 154511 154610: gap of unknown length
* 154611 157925: contig of 3315 bp in length
* 157926 158025: gap of unknown length
* 158026 160712: contig of 2687 bp in length
* 160713 160812: gap of unknown length
* 160813 163479: contig of 2667 bp in length
* 163480 163579: gap of unknown length
* 163580 165744: contig of 2165 bp in length
* 165745 165844: gap of unknown length
* 165845 168563: contig of 2719 bp in length.

FEATURES
    source
        1. 178415
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="1"
            /map="1"

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1730: contig of 1730 bp in length
* 1731 1830: gap of 100 bp
* 1831 4407: contig of 2577 bp in length
* 4408 4507: gap of 100 bp
* 4508 9349: contig of 4842 bp in length
* 9350 9449: gap of 100 bp
* 9450 15955: contig of 6506 bp in length
* 15956 16055: gap of 100 bp
* 16056 20307: contig of 4252 bp in length
* 20308 20407: gap of 100 bp
* 20408 26374: contig of 5967 bp in length
* 26375 26474: gap of 100 bp
* 26475 39624: contig of 13150 bp in length
* 39625 39724: gap of 100 bp
* 39725 57149: contig of 17425 bp in length
* 57150 57249: gap of 100 bp
* 57250 76223: contig of 18974 bp in length
* 76224 76323: gap of 100 bp
* 76324 101233: contig of 24910 bp in length
* 101234 101333: gap of 100 bp
* 101334 132080: contig of 30747 bp in length
* 132081 132180: gap of 100 bp
* 132181 178415: contig of 46235 bp in length.

FEATURES
    source
        1. 178415
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="1"
            /map="1"

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/clone="Rp11-474M18"
/clone_lib="RPC1-11 Human Male BAC"
misc_feature 1..1730
/note="assembly-fragment"
misc_feature 1831..4407
/note="assembly-fragment"
misc_feature 4508..9349
/note="assembly-fragment"
misc_feature 9450..15955
/note="assembly-fragment"
misc_feature 16056..20307
/note="assembly-fragment"
clone_end:SP6
vector_side:left"
misc_feature 20408..26374
/note="assembly-fragment"
misc_feature 26475..39624
/note="assembly-fragment"
clone_end:T7
vector_side:right"
misc_feature 39725..57149
/note="assembly-fragment"
misc_feature 57250..76223
/note="assembly-fragment"
misc_feature 76324..101233
/note="assembly-fragment"
misc_feature 101334..132080
/note="assembly-fragment"
misc_feature 132181..178415
/note="assembly-fragment"
BASE COUNT 60179 a 31444 c 30146 g 55546 t 1100 others
ORIGIN

Query Match 67.3% Score 20.2; DB 2; Length 178415;
Best Local Similarity 88.0%; Pred. No. 4.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 cagcaccgaagtcggatcgagatcc 30
|||||
Db 113773 CAGCACCAATCCACATGCAGATCC 113797

RESULT 37
AB01082S01/c 3194 bp DNA linear PRI 14-APR-2000
LOCUS Homo sapiens MASP gene for mannose binding protein-associated
DEFINITION protease, exon 1.
ACCESSION AB010822
VERSION AB010822.1 GI:3985963
KEYWORDS MASP; mannose binding protein-associated protease.
SEGMENT 1 of 16
SOURCE Homo sapiens DNA, clone_lib:lamda FIX II clone:F419.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Endo, Y.
TITLE Molecular evolution of mannose binding protein-associated serine
protease (MASP)
JOURNAL Unpublished (1998)
AUTHORS 2 (bases 1 to 3194)
TITLE Endo, Y.
JOURNAL Direct Submission
REFERENCE Submitted (28-JAN-1998) Yuichi Endo, Fukushima Medical College,
Dept. of Biochemistry; 1-Hikarigaoka, Fukushima-shi, Fukushima
960-12, Japan (E-mail: yendo@cc.fmu.ac.jp, Tel: 81-245-48-2111,
Fax: 81-245-48-6760)
FEATURES
source
1..3194
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="F419"

5'UTR /clone_lib="lamda FIX II"
2379..2428
/gene="MASP"
exon 2379..2433
/gene="MASP"
/number=1
/product="mannose binding protein-associated protease"
BASE COUNT 877 a 696 c 733 g 888 t
ORIGIN

Query Match 66.7% Score 20; DB 9; Length 3194;
Best Local Similarity 82.1%; Pred. No. 5.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctggcagcaccgaagtcggatcgagatc 28
|||||
Db 1694 CTGGGAGCAGCAGCTCGATGTGCT 1667

RESULT 38
COTLEOC 4943 bp DNA linear PLN 31-MAY-1994
LOCUS Gossypium hirsutum 18.2 kDa oleosin (Matp6-A) gene, complete cds.
DEFINITION L00936
ACCESSION L00936.1 GI:167364
VERSION 18.2 kDa oleosin; membrane protein.
KEYWORDS Gossypium hirsutum (strain Coker 201) DNA.
SOURCE Gossypium hirsutum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Gossypium.

REFERENCE 1 (bases 1 to 4943)
AUTHORS Hughes, D.W., Wang, H.Y. and Galau, G.A.
TITLE Cotton (Gossypium hirsutum) Matp6 and Matp7 oleosin genes
JOURNAL Plant Physiol. 101, 697-698 (1993)
MEDLINE 94105311

FEATURES
source
1..4943
Location/Qualifiers

5'UTR /organism="Gossypium hirsutum"
/strain="Coker 201"
/db_xref="taxon:3635"
/dev_stage="embryos, 20-23 days postanthesis
(preendoreduplication) cotyledon"
gene 3265..3348
/gene="Matp6-A"
/note="putative"
3265..4067
/gene="Matp6-A"
3265..4067
/gene="Matp6-A"
3265..4067
/gene="Matp6-A"
/evidence="experimental"
3349..3855
/gene="Matp6-A"
/note="putative"
/citation=[1]
/codon_start=1
/product="18.2 kDa oleosin"
/protein_id="AA18525.1"
/db_xref="GI:167365"
/translation="MAVYRDRNLPHQYVHPQYRDLNTGGGCGAKNYSRSTSOVL
AVLLPLPGGTLALAGLLTACTVIGMLATPDLFTFSFVLPAIATAMATGFLSS
GAFGLTGLSSLYVILNRLYATGTBOLDLDAKRRVODMTEYVGKTRKVEGOKIENKA
HEGQVGR"
3856..4067
/gene="Matp6-A"
/note="putative"
4042..4047
/gene="Matp6-A"
/note="putative"
4067
/gene="Matp6-A"
/evidence="experimental"
polyA_site
polyA_signal
3'UTR


```

* 207930 210021: contig of 2092 bp in length
* 210022 210121: gap of unknown length
* 210122 212766: contig of 2645 bp in length
* 212767 212866: gap of unknown length
* 212867 215930: contig of 3064 bp in length
* 215931 216030: gap of unknown length
* 216031 218057: contig of 2027 bp in length
* 218058 218157: gap of unknown length
* 218158 219598: contig of 1441 bp in length
* 219599 219698: gap of unknown length
* 219699 222618: contig of 2920 bp in length
* 222619 225859: contig of 3141 bp in length
* 225860 225959: gap of unknown length
* 225960 227832: contig of 1873 bp in length
* 227833 227932: gap of unknown length
* 227933 230488: contig of 2556 bp in length
* 230489 232912: contig of 2324 bp in length
* 230589 232913: gap of unknown length
* 232913 234385: contig of 1373 bp in length
* 234386 234485: gap of unknown length
* 234486 235883: contig of 1398 bp in length
* 235884 237590: contig of 1607 bp in length
* 237591 239482: gap of unknown length
* 239483 239582: contig of 1792 bp in length
* 239583 241021: contig of 1439 bp in length
* 241022 243601: contig of 2480 bp in length
* 243602 243701: gap of unknown length
* 243702 245107: contig of 1406 bp in length
* 245108 245207: gap of unknown length
* 245208 246935: contig of 1728 bp in length
* 246936 247035: gap of unknown length
* 247036 248780: contig of 1745 bp in length
* 248781 250984: gap of unknown length
* 250985 251084: contig of 2104 bp in length
* 251085 252683: contig of 1599 bp in length
* 252684 252783: gap of unknown length
* 252784 253868: contig of 1085 bp in length
* 253869 255016: gap of unknown length
* 255017 255116: contig of 1048 bp in length
* 255117 256306: contig of 1190 bp in length
* 256307 258016: gap of unknown length
* 258017 258116: contig of 1610 bp in length
* 258117 259924: gap of unknown length
* 259925 260024: contig of 1808 bp in length
* 260025 261112: gap of unknown length
* 261113 261212: contig of 1088 bp in length
* 261213 263047: gap of unknown length
* 263048 263147: contig of 1835 bp in length
* 263148 264800: gap of unknown length
* 264801 264900: gap of unknown length
* 264901 266364: contig of 1464 bp in length
* 266365 266464: gap of unknown length
* 266465 267855: contig of 1391 bp in length
* 267856 267955: gap of unknown length
* 267956 269294: contig of 1339 bp in length
* 269295 269394: gap of unknown length
* 269395 270960: contig of 1566 bp in length
* 270961 271060: gap of unknown length
* 271061 272125: contig of 1065 bp in length
* 272126 272225: gap of unknown length
* 272226 273587: contig of 1362 bp in length

```

```

Query Match      66.7%; Score 20; DB 2; Length 275272;
Best Local Similarity 82.1%; Pred. No. 5.1e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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```

QY      1 ctgggcagcaccaagtcggatgcagat 28
        | ||||| ||||| ||||| ||||| |||||
Db 168077 CGGGCAGCAAAAAGTCGGATGCAGAT 168104

RESULT 40
LOCUS   HS157D11R
DEFINITION
H.sapiens Cpg island DNA genomic MseI fragment, clone 157d11,
reverse read cpg157d11.r1a.
ACCESSION 259486
VERSION   259486.1 GI:1031399
KEYWORDS  Cpg island, genomic MseI fragment.
SOURCE   human.
ORGANISM Homo sapiens
           Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Dodsorth,S.J., Huckle,E., Wilkinson,P. and Micklem,G.
TITLE    Direct Submission
JOURNAL  Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RQ, England. E-mail contact: humquerry@sanger.ac.uk
2 (bases 1 to 258)
REFERENCE Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
TITLE    Purification of Cpg islands using a methylated DNA binding column
JOURNAL  Nat. Genet. 6 (3), 236-244 (1994)
MEDLINE  94282070
COMMENT  Vector: pGEM-52f(-)
          Clones are available from the UK MRC Human Genome Mapping Project
          Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
          http://www.hgmp.mrc.ac.uk/ for details
          or contact: biohelp@hgmp.mrc.ac.uk.
          Location/Qualifiers
            source
              1. 258
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /sex="male"
                /dev_stage="adult"
                /tissue_type="blood"
                /clone_lib="CGI-1"
                /clone="157d11"
BASE COUNT 41 a 69 c 91 g 55 t 2 others
ORIGIN
Query Match      65.3%; Score 19.6; DB 9; Length 258;
Best Local Similarity 84.6%; Pred. No. 8.2e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 ctgggcagcaccaagtcggatgcag 26
        | ||||| ||||| ||||| ||||| |||||
Db      67 CTGGCAGCACCAAGTCGGATGCAG 92

RESULT 41
LOCUS   AF254143
DEFINITION
Candida albicans repressed by TUP1 protein 2 (RBT2) gene, complete
cgs.
ACCESSION AF254143
VERSION   AF254143.1 GI:9963983
KEYWORDS  .
SOURCE   Candida albicans.
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
           Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1 (bases 1 to 5883)
AUTHORS  Braun,B.R. and Johnson,A.D.
TITLE    TUP1, CPH1 and EFG1 make independent contributions to filamentation
in candida albicans
JOURNAL  Genetics 155 (1), 57-67 (2000)
MEDLINE  20253093

```

PUBMED 10790384
 REFERENCE 2 (bases 1 to 5883)
 AUTHORS Braun,B.R., Head,W.S., Wang,M.X. and Johnson,A.D.
 TITLE Identification and characterization of TUP1-regulated genes in
 Candida albicans
 JOURNAL Genetics 156 (1), 31-44 (2000)
 MEDLINE 20435724
 PUBMED 10978273
 REFERENCE 3 (bases 1 to 5883)
 AUTHORS Braun,B.R. and Johnson,A.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-APR-2000) Microbiology, UC San Francisco, 513
 Parnassus Ave, S-410, San Francisco, CA 94143-0414, USA

FEATURES
 source
 1..5883
 /organism="Candida albicans"
 /db_xref="taxon:5476"
 1498..3618
 /gene="RBT2"
 1498..3618
 /gene="RBT2"
 /note="feric reductase; contains a predicted signal
 sequence and six transmembrane segments; similar to
 Candida albicans Cflp1 and to Saccharomyces cerevisiae
 Fre2p; Rbt2p"
 /codon_start=1
 /transl_table=12
 /product="repressed by TUP1 protein 2"
 /protein_id="AAG09788.1"
 /db_xref="GI:9963984"
 /translation="WAINSLFLPAITLVSSAQTDTLTTHNKFVAOACKLIGKT
 ALEFNETDKAGFCNVKQALGTMAECIELPHKDSKEFLTKCKNLDEDLAA
 WKNAEEFGYVNTADPDKKKLYKPKLVKKKVEAMDAVATRWYNNYAQWYGLA
 LFSYFAVFAVAGICNLTFPLPFGPVKSLKGISNAFKRYITLPALFKKTAHHSIF
 GQFHAIIPTLESLILVAFIMALIMNLINYYHVKDNYIMPOKSNELGRKIADRTGOI
 SMNLMPPIVLAGRNNFYQWTSNGPYARFYIHKYISRVVNSIAHSGVGTINKEGI
 GYTRRNKPIYRWGIVLVAMSLVFEQSTFERNTYEVFGVHIIIAVRIAGTWI
 HTTEGGYQMMYGAVAVWFDVRVRIARLAFGLRSATVOLIANETVYVTSRPGMWK
 PEPGCHAFIHMRPCTCFWQSHPTIVDSVTSNTITFYIKYGVGTHLYOYLAQPA
 QTAQIKVSIIEGPGNRMAIDRENDVFIAGNGIPIGYEADIKRGEKRNVTLYV
 VVRHRSLEWFIQELTKLDLPISTFYVTOPNGLADPIITDLDDDEOQHEDEK
 SDTESNDYVAVOKNKSFIQFIETKPDFTYQVGEIINQSTGPIAFASCAHGMVDV
 RKSVDNLSNSHRELFEDQMNV"

BASE COUNT 1797 a 1041 c 992 g 2053 t
 ORIGIN

Query Match 65.3%; Score 19.6; DB 8; Length 5883;
 Best Local Similarity 84.6%; Pred. No. 7.9e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 gcagaccacgaatcgatcgatcc 30
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 DB 4656 GCAGCACCGATCCAGATCCAGATCC 4681

RESULT 42
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 LOCUS Homo sapiens chromosome 17 clone RP11-158C19 map 17, LOW-PASS
 DEFINITION
 SEQUENCE SAMPLING.
 AC107940
 VERSION AC107940.1 GI:18308667
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 64116)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 17, clone RP11-158C19
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 64116)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
 Brown,A., Camarata,J., Campioano,A., Chang,J., Chazaro,B.,
 Choquel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearliano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferrelle,P., Fitzhugh,W., Gage,D., Galagan,J., Garday,S.,
 Glinde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,M., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Laroque,K., Lamazares,R.,
 Lander,E., Lechoczky,J., Levine,R., Liu,G., MacLean,C.,
 Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 McEwan,P., McKernan,K., Meldrum,T., Menkus,L., Minova,T.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Ribback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schopback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thoman,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.

TITLE

Direct Submission

COMMENT

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 158_C_19

Center clone name: 158_C_19

NOTE: This record contains 78 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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 735 834: gap of 100 bp
 835 1558: contig of 724 bp in length
 1559 1658: gap of 100 bp
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 2391 2490: gap of 100 bp
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 3301 4033: contig of 733 bp in length
 4034 4133: gap of 100 bp
 4134 4860: contig of 727 bp in length
 4861 4960: gap of 100 bp
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 6501 6600: gap of 100 bp
 6601 7331: contig of 731 bp in length
 7332 7431: gap of 100 bp
 7432 8168: contig of 737 bp in length
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 8995 9094: gap of 100 bp
 9095 9806: contig of 712 bp in length
 9807 9906: gap of 100 bp
 9907 10640: contig of 734 bp in length

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 * 10741 11468: contig of 728 bp in length
 * 11469 11568: gap of 100 bp
 * 11569 12302: contig of 734 bp in length
 * 12303 12402: gap of 100 bp
 * 12403 13148: contig of 746 bp in length
 * 13149 13248: gap of 100 bp
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 * 14099 14817: contig of 719 bp in length
 * 14818 14917: gap of 100 bp
 * 14918 15614: contig of 697 bp in length
 * 15615 15714: gap of 100 bp
 * 15715 16427: contig of 713 bp in length
 * 16428 16527: gap of 100 bp
 * 16528 17250: contig of 723 bp in length
 * 17251 17350: gap of 100 bp
 * 17351 18076: contig of 726 bp in length
 * 18077 18176: gap of 100 bp
 * 18177 18898: contig of 722 bp in length
 * 18899 18998: gap of 100 bp
 * 18999 19731: contig of 733 bp in length
 * 19732 19831: gap of 100 bp
 * 19832 20560: contig of 729 bp in length
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 * 20661 21390: contig of 730 bp in length
 * 21391 21490: gap of 100 bp
 * 21491 22218: contig of 728 bp in length
 * 22219 22318: gap of 100 bp
 * 22319 23019: contig of 701 bp in length
 * 23020 23119: gap of 100 bp
 * 23120 23836: contig of 717 bp in length
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 * 24658 24757: gap of 100 bp
 * 24758 25449: contig of 692 bp in length
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 * 27182 27907: contig of 726 bp in length
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 * 45367 46094: contig of 728 bp in length
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 * 46899 46998: gap of 100 bp
 * 46999 47747: contig of 749 bp in length
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 * 49400 49499: gap of 100 bp
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 * 50317 51036: contig of 720 bp in length
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 * 54327 54426: gap of 100 bp
 * 54427 55128: contig of 702 bp in length
 * 55129 55228: gap of 100 bp
 * 55229 55947: contig of 719 bp in length
 * 55948 56047: gap of 100 bp
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Query Match 65.3%; Score 19.6; DB 2; Length 64116;
 Best Local Similarity 84.6%; Pred. No. 7.6e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 tgggcagcaccacgaatccgagtcgaga 27
 Db 48464 TGGGAGCATCATGTCAGAGATGCAGA 48439

RESULT 43
 LOCUS AC008956 110129 bp DNA linear PRI 21-JUL-2001
 DEFINITION Homo sapiens chromosome 16 clone CTD-2343L5, complete sequence.
 ACCESSION AC008956
 VERSION AC008956.8 GI:14993669
 KEYWORDS HMG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 110129)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 110129)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 110129)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell

REFERENCE	Drive, Walnut Creek, CA 94598, USA									
AUTHORS	4 (bases 1 to 110129)									
TITLE	DOE Joint Genome Institute and Stanford Human Genome Center.									
JOURNAL	Direct Submission									
COMMENT	Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA									
	On Jul 21, 2001 this sequence version replaced gi:14572122.									
	Draft Sequence Produced by DOE Joint Genome Institute									
	www.jgi.doe.gov									
	Finishing Completed at Stanford Human Genome Center									
	www.shgc.stanford.edu									
	Quality: Phrap Quality >=40 99.9% of Sequence;									
	Estimated Total Number of Errors is 0.1.									
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	SHGC-60517 G36854.									
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ORIGIN										
Query Match	65.3%; Score 19.6; DB 9; Length 110129;									
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Matches	22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
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RESULT 44										
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DEFINITION	Homo sapiens Chromosome 16 BAC clone C1987SK-A-761H5, complete sequence.									
ACCESSION	AC002544									
VERSION	AC002544.1 GI:3337382									
KEYWORDS	HTG.									
SOURCE	human.									
ORGANISM	Homo sapiens									
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
REFERENCE	1 (bases 1 to 156641)									
AUTHORS	Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L., Desliartes,M.S., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.									
	Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q									
	Genomics 60 (3), 295-308 (1999)									
TITLE										
JOURNAL										
MEDLINE	99425270									
PUBMED	10493829									
REFERENCE	2 (bases 1 to 156641)									
AUTHORS	Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.									
	Homo sapiens Chromosome 16 BAC clone C1987SK-A-761H5									
TITLE	Unpublished									
JOURNAL	3 (bases 1 to 156641)									
AUTHORS	Adams,M.D. and Loftus,B.J.									
REFERENCE	Direct Submission									
TITLE	Submitted (12-SEP-1997) The Institute for Genomic Research, 9712									
JOURNAL	Medical Center Dr., Rockville, MD 20850, USA, Email:									
	mdamsetl@igr.org									
	4 (bases 1 to 156641)									
REFERENCE	Adams,M.D. and Loftus,B.J.									
AUTHORS	Direct Submission									
TITLE	Submitted (24-JUL-1998) The Institute for Genomic Research, 9712									
JOURNAL	Medical Center Dr., Rockville, MD 20850, USA									

COMMENT
On Jul 24, 1998 this sequence version replaced g1.2595956.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail address: humgent@igrr.org. The orientation of the sequence is from S56 end to 3' end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from athur.gem.ornl.gov), GeneFinder (Phil Green, University of Washington), GENSCAN (Chris Burge, http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (<http://www.tigr.org/tdb/ngi/ngi.html>). Genes without peptide homology having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>) location/unaffiliars

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IPFALLASVFLTLTSPADPGGEEAESARQPLIRTEAPESKPOSSSSLSIREMT
VFGGLIMYVPLVIVVYFAEYFINGLFEFLFEMNTSISHAQRYOMLYOAGVFAFS
SSLRCCRIETRTMALLOCLNLYELADVYFGPLPSYVFLITLIVEGLLGAAYVT
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BASE COUNT 41602 a 38891 c 38211 g 37878 t 59 others
ORIGIN
Query Match 65.3%; Score 19.6; DB 9; Length 156641;
Best Local Similarity 84.6%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ggcagcaccaagtcggatgcagatc 29
Db 66730 GGCAGCACCAAGCCCGGTGGAGCTC 66755
|||||
RESULT 45
AC068137 166719 bp DNA linear PRI 09-JAN-2002
LOCUS
DEFINITION Homo sapiens BAC clone RP11-803A13 from 2, complete sequence.
AC068137
AC068137.8 GI:15375223
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE
AUTHORS Du, H. and Doebber, A.
TITLE The sequence of Homo sapiens BAC clone RP11-803A13
JOURNAL Unpublished (2001)
REFERENCE
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (28-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE
AUTHORS Waterston, R.
TITLE Direct Submission

JOURNAL

COMMENT

Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 30, 2001 this sequence version replaced gi:13570009.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: saplens@wustl.wustl.edu

----- Summary Statistics

Center project name: H_NH0803A13

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPI1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

Actual start of this clone is at base position 1 of RP11-803A13; actual end is at base position 166719 of RP11-803A13.

Sequence derived from PCR from base position 103627 to 103689.

FEATURES

source

1.166719
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-803A13"
 /clone_lib="RPI1-11"
 1074..11102
 /rpt_family="AT-rich"
 1480..2050
 /note="similar to EST A1806700 (NID:g5393266) wfs5f06.x1"
 misc_feature
 1634..2034
 /note="similar to EST D59310 (NID:g960416)"
 repeat_region
 2010..2233
 /rpt_family="ERV1"
 repeat_region
 2234..2745
 /rpt_family="ERV1"
 repeat_region
 2766..2816
 /rpt_family="(CA)n"
 repeat_region
 2869..3044
 /rpt_family="ERV1"
 repeat_region
 3039..3063
 /rpt_family="(A)n"
 repeat_region
 3253..4065
 /rpt_family="L1"
 repeat_region
 4159..4236

/rpt_family="(TA)n"
 4368..4530
 /rpt_family="MER1_type"
 repeat_region
 4555..4582
 /rpt_family="(TTTG)n"
 repeat_region
 4589..4836
 /rpt_family="Alu"
 repeat_region
 5809..6027
 /rpt_family="MIR"
 repeat_region
 6195..6277
 /rpt_family="MER1_type"
 repeat_region
 6281..6328
 /rpt_family="L1"
 repeat_region
 6329..6647
 /rpt_family="Alu"
 repeat_region
 6620..6647
 /rpt_family="(A)n"
 repeat_region
 6648..6728
 /rpt_family="L1"
 misc_feature
 6779..7265
 /note="similar to EST AA576508 (NID:g2354008) nm76c09.s1"
 repeat_region
 6787..6975
 /rpt_family="L2"
 repeat_region
 7307..7356
 /rpt_family="(T)n"
 repeat_region
 7327..7634
 /rpt_family="Alu"
 repeat_region
 7696..8005
 /rpt_family="Alu"
 repeat_region
 7864..7886
 /rpt_family="(T)n"
 misc_feature
 7889..8332
 /note="similar to EST A1625794 (NID:g4650737) ty67d04.x1"
 misc_feature
 8277..8751
 /note="similar to EST BF059443 (NID:g10813261)"
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 9133..9291
 /rpt_family="MIR"
 misc_feature
 9275..9461
 /note="similar to EST AA704040 (NID:g2713958) ag81f10.r1"
 repeat_region
 9616..10006
 /rpt_family="MALR"
 repeat_region
 10039..10130
 /rpt_family="MALR"
 misc_feature
 10299..10638
 /note="similar to EST AA005136 (NID:g1448639) zh95e03.s1"
 misc_feature
 10491..10638
 /note="similar to EST A1078188 (NID:g3412596) cz12f08.x1"
 repeat_region
 10649..11134
 /rpt_family="ERVK"
 misc_feature
 11136..11408
 /note="similar to EST AA005136 (NID:g1448639) zh95e03.s1"
 misc_feature
 11136..11408
 /note="similar to EST A1078188 (NID:g3412596) cz12f08.x1"
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 11333..11414
 /rpt_family="L2"
 repeat_region
 12686..12928
 /rpt_family="L1"
 misc_feature
 12716..13320
 /note="similar to EST AM972049 (NID:g8161790)"
 misc_feature
 13324..13671
 /note="similar to EST BG181175 (NID:g13702947)"
 misc_feature
 13326..13674
 /note="similar to EST AA905838 (NID:g3040961) oj87c08.s1"
 misc_feature
 13842..14185
 /note="similar to EST AA904412 (NID:g3039535) ok07e01.s1"
 misc_feature
 14316..14795
 /note="similar to EST AM293618 (NID:g6700254)"
 misc_feature
 14518..14703
 /note="similar to EST A1352084 (NID:g4089290) qr10b01.x1"
 misc_feature
 14668..15090
 /note="similar to EST A1138580 (NID:g3644552) qd85b12.x1"
 repeat_region
 15359..15906
 /rpt_family="L1"

repeat_region 15945. 16436
/rpt_family="L1"
repeat_region 16406. 16453
/rpt_family="(T)n"
repeat_region 16437. 16566
/rpt_family="Alu"
repeat_region 16567. 17589
/rpt_family="L1"
repeat_region 17590. 17893

Query Match 65.3%; Score 19.6; DB 9; Length 166719;
Best Local Similarity 84.6%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctgggcagcacaagtcgagatgcag 26
|||||
Db 163688 CTGGGCAGCACCAAGCGCGGTGCAG 163713

Search completed: September 10, 2002, 01:47:23
Job time: 6170 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 00:38:51 : Search time 211.16 seconds
(without alignments)
243.926 Million cell updates/sec

Title: US-09-912-436-5_COPY_275_304

Perfect score: 30
Sequence: 1 ctggcgcagcaccacgaicccgatgcagatcc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472854

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99%

Listing first 45 summaries

Database : N.Geneseq_032802:*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27.4	91.3	910	17 AAT33613	Vascular endothelial
2	27	90.0	531	21 AAA15763	DNA encoding VEGF-
3	26.8	89.3	405	17 AAT37912	VEGF-B112 coding s
4	26.8	89.3	405	17 AAV63566	CDNA clone encodin
5	26.8	89.3	565	17 AAT37910	Adult heart VEGF-B
6	26.8	89.3	565	20 AAV63564	CDNA clone encodin
7	26.8	89.3	624	17 AAT37914	VEGF-B186 coding s
8	26.8	89.3	624	20 AAV63568	CDNA clone encodin
9	26.8	89.3	624	22 AAC81776	Human vascular end

10	26.8	89.3	624	22 AAC81777	Murine vascular en
11	26.8	89.3	886	17 AAT37909	Partial VEGF-B cod
12	26.8	89.3	886	20 AAV63563	CDNA clone encodin
13	26.8	89.3	1141	17 AAT13810	Murine VRF167 CDNA
14	26.8	89.3	1242	17 AAT13809	Murine VRF186 CDNA
15	26	86.7	445	21 AAA15764	DNA encoding VEGF-
16	23.6	78.7	591	17 AAT37911	Adult heart VEGF-B
17	23.6	78.7	591	20 AAV63565	CDNA clone encodin
18	22.2	74.0	423	21 AAA15766	DNA encoding VEGF-
19	20.8	69.3	389	21 AAA15881	DNA encoding a hom
20	20.6	68.7	2002	22 AAK66306	Human immune/haema
21	20.6	68.7	2205	22 AAK66307	Human immune/haema
22	20.6	68.7	22680	22 AAK66308	Human immune/haema
23	20.6	68.7	22680	22 AAK73334	Human immune/haema
24	20.6	68.7	22680	22 AAK73344	Human immune/haema
25	20.6	68.7	22680	22 AAK73625	Human immune/haema
26	20.6	68.7	22680	22 AAK73847	Human immune/haema
27	20.6	68.7	22680	22 AAK73934	Human immune/haema
28	20.6	68.7	22680	22 AAK78350	Human immune/haema
29	19.6	65.3	197	22 ABA70982	Human foetal liver
30	19.6	65.3	197	22 ABA37402	Probe #15868 for g
31	19.6	65.3	197	22 AAK19258	Human brain expres
32	19.6	65.3	197	22 AAK45228	Human bone marrow
33	19.6	65.3	197	22 AAI25200	Probe #15133 for g
34	19.6	65.3	197	22 AAI51179	Probe #19865 used
35	19.6	65.3	486	22 ABA58386	Human foetal liver
36	19.6	65.3	486	22 ABA27497	Probe #5963 for ge
37	19.6	65.3	486	22 AAK06491	Human brain expres
38	19.6	65.3	486	22 AAK32172	Human bone marrow
39	19.6	65.3	486	22 AAI15983	Probe #5916 for ge
40	19.6	65.3	486	22 AAI38021	Probe #6707 used t
41	19.4	64.7	1956	19 AAV02897	Murine Ena-VASP li
42	19.4	64.7	7885	22 AAK70210	Human immune/haema
43	19.2	64.0	2687	22 ABL07968	Drosophila melanog
44	19	63.3	1882	23 AAH26807	Mouse osteoregulin
45	19	63.3	8438	15 AAQ73500	DNA encoding Pseud

ALIGNMENTS

RESULT 1	
ID AAT33613	standard; cDNA; 910 bp.
XX AAT33613;	
AC	
XX	
DT 30-NOV-1996	(first entry)
XX	
DE Vascular endothelial growth factor-1 like protein SOM175-e4 CDNA.	
XX	
KW Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;	
KW astroglial proliferation; ss.	
XX	
OS Homo sapiens.	
XX	
EH Key	Location/Qualifiers
FT CDS	3..308
FT	/*tag= a
FT	sig-peptide
FT	3..65
FT	/*tag= b
FT	mat-peptide
FT	66..305
XX	/*tag= c
PN	
W09627007-A1.	
XX	
PD 06-SEP-1996.	
XX	
PF 22-FEB-1996;	96WO-AU00094.
XX	
PR 22-DEC-1995;	95AU-0007274.
PR 02-MAR-1995;	95AU-0001457.
PR 20-NOV-1995;	95AU-0006647.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.
PA
XX
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
XX
XX WPI: 1996-412774/41.
DR P-PSDB: AAM00738.
XX
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
XX
PS Example 3: Page 47-48; 113pp; English.
XX
CC 3 CDNA clones (AA13611-13) code for splice variants (AAM00726-28)
CC of the human vascular endothelial growth factor-like polypeptide
CC SOM175 (see also AAM00725). They were identified in a human foetal
CC spleen library and respectively lack exon 6, exons 6+7, and exon 4
CC of the SOM175 gene (see also AA13610). The CDNA clones can be
CC used to produce recombinant SOM175 proteins that are useful for
CC inducing astroglial proliferation and for promoting neural survival
CC and/or proliferation.
XX
SQ Sequence 910 BP; 182 A; 316 C; 254 G; 158 T; 0 other;

Query Match 91.3%; Score 27.4; DB 17; Length 910;
Best Local Similarity 96.6%; Pred. No. 0.03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctggcagcagcaccagtcgcgagtcgagacc 29
|||||
Db 277 ctggcagcagcaccagtcgcgagtcgagacc 305

RESULT 2
AA15763
ID AA15763 standard; DNA; 531 BP.
XX
XX AA15763:
AC
XX
XX 19-JUN-2000 (first entry)
XX
XX DNA encoding VEGF-3 homologue, SEQ ID NO:21.
XX
XX Vascular endothelial growth factor 3; VEGF-3; homologue;
KW vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200009148-A1.
PN
XX
XX 24-FEB-2000.
PD
XX
XX 10-AUG-1999; 99WO-US18054.
PF
XX
XX 10-AUG-1998; 98US-0132088.
PR
XX
XX 10-FEB-1999; 99US-0244694.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Hu J, Olsen HS, Rosen CA;
PI
XX
XX WPI: 2000-224173/19.
DR

PT New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
PT disorders associated with vascular and lymphatic system -
XX
XX Disclosure; Page 137; 209pp; English.

CC The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AAY4802), a splice variant of human VEGF-3 (AAY94806), and
CC nucleic acids encoding them (AA15748, AA15762). The CDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line CDNA library.
CC The CDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. Sequences AA15761-AA1580 represent DNA
CC sequences encoding homologues of human VEGF-3 from human, mouse and rat.
XX
SQ Sequence 531 BP; 111 A; 162 C; 163 G; 95 T; 0 other;

Query Match 90.0%; Score 27; DB 21; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcgcgagtcgagacc 30
|||||
Db 191 ggcagcaccagtcgcgagtcgagacc 217

RESULT 3
AA137912
ID AA137912 standard; CDNA; 405 BP.
XX
XX AA137912:
AC
XX
XX 28-APR-1997 (first entry)
XX
XX VEGF-B112 coding sequence.
XX
XX
XX Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse; ss.
XX
XX Mus musculus.
OS
XX
XX WO9626736-A1.
PN
XX
XX 06-SEP-1996.
PD
XX
XX 01-MAR-1996; 96WO-US02957.
PF
XX
XX 06-DEC-1995; 95US-0569063.
PR
XX
XX 01-MAR-1995; 95US-0397651.
PR
XX
XX 06-JUN-1995; 95US-0469427.
PR
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI
XX
XX Alitalo K, Eriksson U, Olofsson B, Pajusola K;
PI
XX
XX WPI: 1996-412582/41.
DR
XX
XX P-PSDB: AAM04828.
DR

PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
XX Claim 1; Page 57; 107pp; English.

CC AAT37909-T37915 represent the coding sequences for the vascular
 CC endothelial growth factor (VEGF) proteins of the invention, which promote
 CC glycosylated cationic dimer, and is sometimes referred to as vascular
 CC permeability factor (VPF). VEGF has diverse effects, depending on the
 CC specific biological context in which it is found. VEGF is a potent
 CC angiogenesis in vivo by promoting endothelial cell growth during normal
 CC embryonic development, wound healing, and tissue
 CC regeneration/reorganisation. The VEGF proteins of the invention share
 CC the angiogenic and other properties of VEGF, but are distributed and
 CC expressed in tissues differently to VEGF. The proteins can therefore be
 CC used to accelerate angiogenesis in wound healing. Antibodies against the
 CC proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.

SQ Sequence 405 BP; 93 A; 113 C; 120 G; 79 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 405;
 Best Local Similarity 93.3%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctgggcagacacacgaagtcgcgagtcgacatcc 30
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 278 ctgggcagacacacgaagtcgcgagtcgacatcc 307

RESULT 4

AAV63566
 ID AAV63566 standard; cDNA; 405 BP.

AC AAV63566;

DT 29-JAN-1999 (first entry)

DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B112.

KM Vascular endothelial growth factor; VEGF; proliferation; mouse;

KW endothelial cell; angiogenesis; tissue growth; organ repair; ss.

XX Mus sp.

OS Location/Qualifiers

FT Key 4..405

FT CDS /tag= a

FT /product= VEGF-B112

PN US5840693-A.

PD 24-NOV-1998.

XX 01-MAR-1996; 9605-0609443.

XX 01-MAR-1996; 9605-0609443.

PR 01-MAR-1996; 9605-0609443.

PR 01-MAR-1995; 9505-0397651.

PR 06-JUN-1995; 9505-0469427.

PR 06-DEC-1995; 9505-0569063.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Altalo K, Eriksson U, Olofsson B, Pajusola K;

XX WPI; 1999-034079/03.

XX P-PDB; AAW04826.

PT Vascular endothelial growth factor-B isoforms, and DNA encoding
 PT them - useful for inducing angiogenesis and cellular proliferation,
 PT and raising antibodies to inhibit activities in e.g. tumours

PS Claim 22; Fig 7; 52pp; English.

XX The present sequence encodes murine vascular endothelial growth factor
 CC (VEGF)-B112. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries form pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.

SQ Sequence 405 BP; 93 A; 113 C; 120 G; 79 T; 0 other;

Query Match 89.3%; Score 26.8; DB 20; Length 405;
 Best Local Similarity 93.3%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctgggcagacacacgaagtcgcgagtcgacatcc 30
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 278 ctgggcagacacacgaagtcgcgagtcgacatcc 307

RESULT 5

AAT37910
 ID AAT37910 standard; cDNA; 565 BP.

AC AAT37910;

DT 28-APR-1997 (first entry)

DE Adult heart VEGF-B167 coding sequence.

KM Endothelial cell; proliferation; vascular endothelial growth factor; VPF;

KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;

KM Vascular permeability factor; cell mitogen; angiogenesis; cell growth;

KW embryonic development; wound healing; tissue reorganisation; antibody;

KM cancer; metastatic risk; tumour cell; mouse; ss.

XX Mus musculus.

OS WO9626736-A1.

PN WO9626736-A1.

PD 06-SEP-1996.

XX 01-MAR-1996; 9605-0502957.

XX 06-DEC-1995; 9505-0569063.

PR 01-MAR-1995; 9505-0397651.

PR 06-JUN-1995; 9505-0469427.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Altalo K, Eriksson U, Olofsson B, Pajusola K;

XX WPI; 1996-412562/41.

XX P-PDB; AAW04826.

XX Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis

PS Claim 1; Page 54-55; 107pp; English.

XX AAT37909-T37915 represent the coding sequences for the vascular

endothelial growth factor (VEGF) proteins of the invention, which promote endothelial or mesodermal cell proliferation. VEGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VEGF has diverse effects, depending on the specific biological context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenesis *in vivo* by promoting endothelial cell growth during normal embryonic development, wound healing, and tissue regeneration/reorganisation. The VEGF proteins of the invention share the angiogenic and other properties of VEGF, but are distributed and expressed in tissues differently to VEGF. The proteins can therefore be used to accelerate angiogenesis in wound healing. Antibodies against the proteins can be used for inhibiting angiogenesis. The antibodies can also be used diagnostically to quantitatively detect VEGF-B. Primers complementary to the coding sequences for the proteins of the invention can also be used to detect VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy specimens may be useful as an indicator of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences directed against the VEGF coding sequences, this is especially useful in retarding VEGF expression in tumour cells.

Query Match	89.3%	Score 26.8	DB 17	Length 565
Best Local Similarity	93.3%	Pred. No. 0.05		
Matches 28; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	ctggcgacgacccaagtcgcgatgcagatcc	30
Db	273	ctggcgacacccaagtcgcgatgcagatcc	302

RESULT	5
AAV63564	
ID	AAV63564 standard; cDNA; 565 BP.

AC AAV63564;

DT 29-JAN-1999 (first entry)

DE CDNA clone encoding vascular endothelial growth factor (VEGF)-B167.

KM Vascular endothelial growth factor; VEGF; proliferation; mouse;
KW endothelial cell; angiogenesis; tissue growth; organ repair; ss

Mus sp.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
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6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
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15	15	15
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19	19	19
20	20	20
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27	27	27
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88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
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98	98	98
99	99	99
100	100	100

FT /*tag= a

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FTT
/transl_except= (pos:1, aa: Met)
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PN US5840693-A.

PD 24-NOV-1998.

PF 01-MAR-1996; 96US-0609443

PR 01-MAR-1996; 96US-0609443

PR 06-JUN-1995; 95US-0469427

XX

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;

DR WPI; 1999-034079/03.

XX

Vascular endothelial growth factor-B iso-forms, and DNA encoding them -- useful for inducing angiogenesis and cellular proliferation, and raising antibodies to inhibit activities in e.g. tumours

Claim 22; Fig 3; 52pp; English.

The present sequence encodes murine vascular endothelial growth factor (VEGF)-B167. VEGF proteins are used for promoting proliferation of endothelial cells and for stimulating angiogenesis (the proliferation of new capillaries from pre-existing blood vessels). These activities are useful for treating tissue growth and repair, including organ repair. This is also useful in pregnancy, in follicle development, as these processes must occur in development of the placenta. The proteins can also be used to raise antibodies, either for use in detection of the proteins or as inhibitors of their action. This is especially useful as angiogenesis is required by tumours as they need new blood supplies to grow and proliferate.

Sequence 565 BP; 120 A; 179 C; 166 G; 100 T; 0 other;

Query Match	89.3%	Score	26.8	DB	20	Length	565
Best Local Similarity	93.3%	Pred. No.	0.05				
Matches	28	Conservative	0	Mismatches	2	Indels	0
						Gaps	0

QY	1	ctggcgagcacc	aagtc	ccgatgc	agatcc	30
Db	273	ctggcgacaccca	aagtc	ccgatgc	agatcc	302

RESULT	7
AAT37914	
ID	AAT37914 standard; cDNA; 624 BP.

AC AAT37914;

DT 28-APR-1997 (first entry)

DE VEGF-B186 coding sequence.

KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;

KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;

KW cancer; metastatic risk; tumour cell; mouse; ss.

OS Mus musculus.

PN W09626736-A1.

PD 06-SEP-1996.

PF 01-MAR-1996; 96WO-US02957.

PR 06-DEC-1995; 95US-0569063.

PR 06-JUN-1995; 95US-0469427.

PA (LUDW-) LUDWIG INST CANCER RES.

XX

XX

DR P-PSDB; AAW04830.

PT Vascular endothelial growth factor VEGF-B proteins - useful to

PT and antibodies for cancer diagnosis

PS Claim 1; Page 60; 107pp; English.

CC AAT37909-T37915 represent the coding sequences for the vascular

CC endothelial growth factor (VEGF) proteins of the invention, which promote
CC endothelial or mesodermal cell proliferation. VEGF is also a
CC glycosylated cationic dimer, and is sometimes referred to as vascular
CC permeability factor (VPF). VEGF has diverse effects, depending on the
CC specific biological context in which it is found. VEGF is a potent
CC endothelial cell mitogen, and directly contributes to induction of
CC angiogenesis in vivo by promoting endothelial cell growth during normal
CC embryonic development, wound healing, and tissue
CC regeneration/reorganisation. The VEGF proteins of the invention share
CC the angiogenic and other properties of VEGF, but are distributed and
CC expressed in tissues differently to VEGF. The proteins can therefore be
CC used to accelerate angiogenesis in wound healing. Antibodies against the
CC proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences directed against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.

XX SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.051;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccacgaatccgagtcagatcc 30
||||| ||||||| ||||||| |||||||
DB 275 ctgggcacaccacgaatccgagtcagatcc 304

RESULT 8
AAV63568
ID AAV63568 standard; cDNA; 624 BP.
XX AC AAV63568;
XX DT 29-JAN-1999 (first entry)
XX DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B186.
XX KM Vascular endothelial growth factor; VEGF; proliferation; mouse;
XX KM endothelial cell; angiogenesis; tissue growth; organ repair; ss.
XX OS Mus sp.
XX FH Key
XX FT CDS Location/Qualifiers
FT 1..624
FT /*tag= a
FT /product= VEGF-B186
XX PN US5840693-A.
XX PD 24-NOV-1998.
XX PF 01-MAR-1996; 96US-0609443.
XX PR 01-MAR-1996; 96US-0609443.
XX PR 01-MAR-1995; 95US-0397651.
XX PR 06-JUN-1995; 95US-0468427.
XX PR 06-DEC-1995; 95US-0565063.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
XX DR WPI; 1999-034079/03.
XX DR P-PSDB; AAM80494.
XX PT Vascular endothelial growth factor-B iso:forms, and DNA encoding

PT them - useful for inducing angiogenesis and cellular proliferation,
PT and raising antibodies to inhibit activities in e.g. tumours
XX PS Claim 22; Fig 12; 52pp; English.
XX XX

CC The present sequence encodes murine vascular endothelial growth factor
CC (VEGF)-B186. VEGF proteins are used for promoting proliferation of
CC endothelial cells and for stimulating angiogenesis (the proliferation
CC of new capillaries form pre-existing blood vessels). These activities
CC are useful for treating tissue growth and repair, including organ
CC repair. This is also useful in pregnancy, in follicle development,
CC as these processes must occur in development of the placenta. The
CC proteins can also be used to raise antibodies, either for use in
CC detection of the proteins or as inhibitors of their action. This is
CC especially useful as angiogenesis is required by tumours as they need
CC new blood supplies to grow and proliferate.

XX SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;

Query Match 89.3%; Score 26.8; DB 20; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.051;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagcaccacgaatccgagtcagatcc 30
||||| ||||||| ||||||| |||||||
DB 275 ctgggcacaccacgaatccgagtcagatcc 304

RESULT 9
AAC81776
ID AAC81776 standard; DNA; 624 BP.
XX AC AAC81776;
XX DT 23-FEB-2001 (first entry)
XX DE Human vascular endothelial growth factor VEGF-B186 coding sequence.
XX KM Human; vascular endothelial growth factor; VEGF-B; bone growth;
XX KM angiogenesis; neovascularisation; bone break; inflammation; ds.
XX OS Homo sapiens.
XX XX WO200064261-A1.
XX PN 02-NOV-2000.
XX PD 26-APR-2000; 2000MO-US11096.
XX PF 26-APR-1999; 99US-0130935.
XX PR 26-APR-1999; 99US-0130935.
XX XX (LUDW-) LUDWIG INST CANCER RES.
XX PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX PI Aase K, Kaipainen A, Olofsson B, Alitalo K, Eriksson U;
XX DR WPI; 2001-015797/02.
XX DR P-PSDB; AAB36296.
XX PT Use of a polypeptide having the biological activity of vascular
XX PT endothelial growth factor-B for stimulating angiogenesis of bone,
XX PT healing of bone fractures and enhancing acceptance of an implant to
XX PT bone
XX PS Disclosure; Page 36-37; 43pp; English.
XX PS The present invention discloses a use for human vascular endothelial
XX CC growth factor B (VEGF-B) in the stimulation of angiogenesis in bone. This
XX CC can be used to promote bone growth, stimulate the healing of breaks or
XX CC fractures, secure an implant to the bone and to alleviate inflammation in
XX CC long bones.

SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;

Query Match
Best Local Similarity 89.3%; Score 26.8; DB 22; Length 624;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagaccagtcgcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 275 ctgggcagaccagtcgcgatgcagatcc 304

RESULT 10
AAC81777
ID AAC81777 standard; cDNA; 624 BP.
XX
AC AAC81777;
XX
DT 23-FEB-2001 (first entry)
XX
DE Murine vascular endothelial growth factor VEGF-B186 coding sequence.
XX
KM Mouse; vascular endothelial growth factor; VEGF-B; bone growth;
KM angiogenesis; neovascularisation; bone break; inflammation; ss.
XX
OS Mus sp.
XX
PN W0200064261-A1.
XX
PD 02-NOV-2000.
XX
PE 26-APR-2000; 2000WO-US1096.
XX
PR 26-APR-1999; 99US-0130935.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI Aase K, Kaipainen A, Olofsson B, Alltalo K, Eriksson U;
XX
DR WPI: 2001-015797/02.
XX
PT Use of a polypeptide having the biological activity of vascular
PT endothelial growth factor-B for stimulating angiogenesis of bone,
PT healing of bone fractures and enhancing acceptance of an implant to
PT bone -
XX
PS Disclosure; Page 38-39; 43pp; English.
XX
CC The present invention discloses a use for human vascular endothelial
CC growth factor B (VEGF-B) in the stimulation of angiogenesis in bone. This
CC can be used to promote bone growth, stimulate the healing of breaks or
CC fractures, secure an implant to the bone and to alleviate inflammation in
CC long bones.
XX
SQ Sequence 624 BP; 124 A; 213 C; 173 G; 114 T; 0 other;

Query Match
Best Local Similarity 89.3%; Score 26.8; DB 22; Length 624;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctgggcagaccagtcgcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 275 ctgggcagaccagtcgcgatgcagatcc 304

RESULT 11
AAT37909
ID AAT37909 standard; cDNA; 886 BP.
XX
AC AAT37909;
XX

DT 28-APR-1997 (first entry)
XX
DE Partial VEGF-B coding sequence.
XX
KM Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KM VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KM vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KM embryonic development; wound healing; tissue reorganisation; antibody;
KM cancer; metastatic risk; tumour cell; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FH CDS 2..312
FT /*tag= a
FT /product= First reading frame VEGF-B fragment
FT CDS 312..479
FT /*tag= b
FT /product= Second reading frame VEGF-B fragment
XX
PN W09626736-A1.
XX
PD 06-SEP-1996.
XX
PE 01-MAR-1996; 96WO-US02957.
XX
PR 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alltalo K, Eriksson U, Olofsson B, Rajusola K;
XX
DR WPI: 1996-412582/41.
DR P-PSDB: AAW04824, AAW04825.
XX
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
PS Claim 1; Page 53; 107pp; English.
XX
CC This represents a fragment of the mouse embryo vascular endothelial
CC growth factor-B (VEGF-B) protein coding sequence. The encoded proteins
CC (and AAW04825-W04831) represent the VEGF proteins of the invention, and
CC promote endothelial or mesodermal cell proliferation. VEGF is also a
CC glycosylated cationic dimer, and is sometimes referred to as vascular
CC permeability factor (VPF). VEGF has diverse effects, depending on the
CC specific biological context in which it is found. VEGF is a potent
CC endothelial cell mitogen, and directly contributes to induction of
CC angiogenesis in vivo by promoting endothelial cell growth during normal
CC embryonic development, wound healing, and tissue
CC regeneration/reorganisation. The VEGF proteins of the invention share
CC the angiogenic and other properties of VEGF, but are distributed and
CC expressed in tissues differently to VEGF. The proteins can therefore be
CC used to accelerate angiogenesis in wound healing. Antibodies against
CC the proteins can be used for inhibiting angiogenesis. The antibodies
CC can also be used diagnostically to quantitatively detect VEGF-B.
CC Primers complementary to the coding sequences for the proteins of the
CC invention can also be used to detect VEGF-B coding sequences.
CC Identification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences, this is especially useful in retarding VEGF expression in
CC tumour cells.
XX
SQ Sequence 886 BP; 227 A; 261 C; 226 G; 172 T; 0 other;

Query Match
Best Local Similarity 89.3%; Score 26.8; DB 17; Length 886;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

[illegible]

Query Match 89.3%; Score 26.8; DB 17; Length 1141;
 Best Local Similarity 93.3%; Pred. No. 0.056;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcgcatgcagatcc 30
 ||||||| ||||||| ||||||| |||||||
 Db 440 ctgggcagcaccaagtcgcatgcagatcc 469

RESULT 14

AA13809
 ID AA13809 standard; cDNA; 1242 BP.

AC AAT13809;
 DT 30-NOV-1996 (first entry)

DE Murine VRF186 cDNA.

XX VRF; vascular endothelial growth factor; VEGF; SOM175; neuron;
 KM astroglial proliferation; ss.
 XX

OS Mus musculus.

XX Key Location/Qualifiers

FT CDS 166..789

FT sig_peptide 166..228

FT mat_peptide 229..786

FT exon 576..676

FT repeat_region 1163..1176

FT polyA_signal /note="polymorphic AC repeat region"
 1186..1191

FT /tag= f

PN MO9627007-A1.

XX 06-SEP-1996.

XX 22-FEB-1996; 96WO-AU00094.

XX 22-DEC-1995; 95AU-0007274.

PR 02-MAR-1995; 95AU-0001457.

PR 20-NOV-1995; 95AU-0006647.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;

PI Weber G;

XX WPI: 1996-412774/41.

DR P-PSDB: AAM00863.

XX New growth factor related to vascular endothelial growth factor -

PT useful for inducing astroglial proliferation and promoting neuronal

PT survival

XX Example 5; Fig 9; 113pp; English.

CC VRF186 cDNA (AA13809) codes for the murine homologue (AAM00863) of
 CC human vascular endothelial growth factor-like polypeptide SOM175
 CC (AAM00725), a protein capable of inducing astroglial proliferation
 CC and of promoting neural survival and/or proliferation. It was
 CC obt'd. from a new-born mouse brain cDNA library using SOM175 cDNA
 CC (see also AA133610) as probe. The murine VRF gene maps near to the
 CC centromere of chromosome 19. It is highly expressed in embryo tissue
 CC and in the heart and brown fat of adult mice. An alternatively

CC spliced variant, VRF169 (AA13810), was also identified.
 XX
 SO Sequence 1242 BP; 272 A; 409 C; 333 G; 228 T; 0 other;

Query Match 89.3%; Score 26.8; DB 17; Length 1242;
 Best Local Similarity 93.3%; Pred. No. 0.057;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcgcatgcagatcc 30
 ||||||| ||||||| ||||||| |||||||
 Db 440 ctgggcagcaccaagtcgcatgcagatcc 469

RESULT 15

AA15764
 ID AA15764 standard; DNA; 445 BP.

AC AA15764;

DT 19-JUN-2000 (first entry)

DE DNA encoding VEGF-3 homologue, SEQ ID NO:22.

XX Vascular endothelial growth factor 3; VEGF-3; homologue;

KM vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;

KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.

XX Homo sapiens.

XX WO200009148-A1.

PD 24-FEB-2000.

PF 10-AUG-1999; 99WO-US18054.

PR 10-AUG-1998; 98US-0132088.

PR 10-FEB-1999; 99US-0244694.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Hu J, Olsen HS, Rosen CA;

PI WPI: 2000-224173/19.

XX New human gene encoding vascular endothelial growth factor 3 and

PT polypeptide encoded by the gene is useful for treating various

PT disorders associated with vascular and lymphatic system -

XX Disclosure; Page 137-138; 209pp; English.

XX The invention relates to human vascular endothelial growth factor 3

CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806) and

CC nucleic acids encoding them (AA15748, AA15762). The cDNA encoding

CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.

CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in

CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3

CC is also expressed in colon, heart, kidney and ovary tissues, this pattern

CC being consistent with vascular and lymphatic specific expression. VEGF-3

CC proteins and nucleotides are useful in preventing, treating or the

CC ameliorating various disorders and conditions associated with the

CC vascular and lymphatic systems. These conditions and disorders include

CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart

CC disease. VEGF-3 may also be used to identify its own binding partners.

CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as

CC an alternative to restriction fragment length polymorphism (RFLP). The

CC nucleotides are also useful to prepare PCR primers for amplifying an

CC isolating selected DNAs. Sequences AA15763-A15880 represent DNA

CC sequences encoding homologues of human VEGF-3 from human, mouse and rat.

XX Sequence 445 BP; 86 A; 170 C; 120 G; 69 T; 0 other;

Query Match 86.7%; Score 26; DB 21; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gcagcaccagtcgcgatgcagatcc 30
 ||||||||||||||||||
 DB 79 gcagcaccagtcgcgatgcagatcc 104

RESULT 16

AAAT37911
 ID AAAT37911 standard; cDNA; 591 BP.

AC AAAT37911;

DT 28-APR-1997 (first entry)

DE Adult heart VEGF-B174 coding sequence.

KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse; ss.

OS Mus musculus.

PN WO9626736-A1.

PD 06-SEP-1996.

PF 01-MAR-1996; 96WO-US02957.

XX 06-DEC-1995; 95US-0569063.

PR 01-MAR-1995; 95US-0397651.

PR 06-JUN-1995; 95US-0469427.

XX (LUDM-) LUDMIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Altalo K, Eriksson U, Olofsson B, Pajusola K;

DR WPI: 1996-412582/41.

DR P-PSDB: AAM04827.

XX Vascular endothelial growth factor VEGF-B proteins - useful to

PT accelerate angiogenesis in wound healing, also related nucleic acid

XX and antibodies for cancer diagnosis

PS Claim 1; Page 56; 107bp; English.

XX AAAT37909-T37915 represent the coding sequences for the vascular
 CC endothelial growth factor (VEGF) proteins of the invention, which promote
 CC endothelial or mesodermal cell proliferation. VEGF is also a
 CC glycosylated cationic dimer, and is sometimes referred to as vascular
 CC permeability factor (VPF). VEGF has diverse effects, depending on the
 CC specific biological context in which it is found. VEGF is a potent
 CC angiogenesis in vivo by promoting endothelial cell growth during normal
 CC embryonic development, wound healing, and tissue
 CC regeneration/reorganisation. The VEGF proteins of the invention share
 CC the angiogenic and other properties of VEGF, but are distributed and
 CC expressed in tissues differently to VEGF. The proteins can therefore be
 CC used to accelerate angiogenesis in wound healing. Antibodies against the
 CC proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.

SO Sequence 591 BP; 126 A; 186 C; 174 G; 105 T; 0 other;

Query Match 78.7%; Score 23.6; DB 17; Length 591;
 Best Local Similarity 86.7%; Pred. No. 1.2;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctggcagcaccagtcgcgatgcagatcc 30
 ||||||| ||||||| ||||||| ||||||| ||
 DB 278 ctggcagcaccagtcgcgatgcagatcc 307

RESULT 17

AAV63565
 ID AAV63565 standard; cDNA; 591 BP.

AC AAV63565;

DT 29-JAN-1999 (first entry)

DE cDNA clone encoding vascular endothelial growth factor (VEGF)-B174.

KW Vascular endothelial growth factor; VEGF; proliferation; mouse;
 KW endothelial cell; angiogenesis; tissue growth; organ repair; ss.

OS Mus sp.

PN US5840693-A.

PD 24-NOV-1998.

PF 01-MAR-1996; 96US-0609443.

XX 01-MAR-1996; 96US-0609443.

PR 01-MAR-1995; 95US-0397651.

PR 06-JUN-1995; 95US-0469427.

XX 06-DEC-1995; 95US-0569063.

XX (LUDM-) LUDMIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Altalo K, Eriksson U, Olofsson B, Pajusola K;

DR WPI: 1999-034079/03.

DR P-PSDB: AAM80491.

XX Vascular endothelial growth factor-B isoforms, and DNA encoding

PT them - useful for inducing angiogenesis and cellular proliferation,

XX and raising antibodies to inhibit activities in e.g. tumours

PS Claim 22; Fig 5; 52bp; English.

XX The present sequence encodes murine vascular endothelial growth factor
 CC (VEGF)-B174. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries form pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.

CC Sequence 591 BP; 126 A; 186 C; 174 G; 105 T; 0 other;

XX Query Match 78.7%; Score 23.6; DB 20; Length 591;

Best Local Similarity 86.7%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctggagcagcacaagtcgcgatgcagatcc 30
||||| ||||||| ||||||| |||
DB 278 ctggagcacaacacagtcgcgatgcagatcc 307

RESULT 18
AAAI5766
ID AAAI5766 standard: DNA; 423 BP.

AAAI5766;

19-JUN-2000 (first entry)

DE DNA encoding VEGF-3 homologue, SEQ ID NO:24.

XX Vascular endothelial growth factor 3; VEGF-3; homologue;
KW vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.

XX Mus musculus.

XX WO200009148-A1.

XX 24-FEB-2000.

XX 10-AUG-1999; 99WO-US18054.

XX 10-AUG-1998; 98US-0132088.

XX 10-FEB-1999; 99US-0244694.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Hu J, Olsen HS, Rosen CA;

XX WPI; 2000-224173/19.

PT New human gene encoding vascular endothelial growth factor 3 and
polypeptide encoded by the gene is useful for treating various
disorders associated with vascular and lymphatic system -

XX Disclosure: Page 139-140; 209pp; English.

XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AA194802), a splice variant of human VEGF-3 (AA194806), and
CC nucleic acids encoding them (AAAI5748, AA15762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. Sequences AA15763-AA15880 represent DNA
CC sequences encoding homologues of human VEGF-3 from human, mouse and rat.
XX

XX Sequence 423 BP; 96 A; 135 C; 123 G; 69 T; 0 other;

Query Match 74.0%; Score 22.2; DB 21; Length 423;
Best Local Similarity 88.9%; Pred. No. 4.4;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 ggcagcacaagtcgcgatgcagatcc 30
||| ||||||| ||||||| |||

DB 52 gggacaacacagtcgcgatgcagatcc 78

RESULT 19

AAAI5881
ID AAAI5881 standard: DNA; 389 BP.

AAAI5881;

19-JUN-2000 (first entry)

DE DNA encoding a homologue of VEGF-3 splice variant, SEQ ID NO:139.

XX Vascular endothelial growth factor 3; VEGF-3; splice variant; homologue;
KW vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
KW cancer; wounds; autoimmune disease; HIV; inflammation; heart disease; ds.

XX Mus musculus.

XX WO200009148-A1.

XX 24-FEB-2000.

XX 10-AUG-1999; 99WO-US18054.

XX 10-AUG-1998; 98US-0132088.

XX 10-FEB-1999; 99US-0244694.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Hu J, Olsen HS, Rosen CA;

XX WPI; 2000-224173/19.

PT New human gene encoding vascular endothelial growth factor 3 and
polypeptide encoded by the gene is useful for treating various
disorders associated with vascular and lymphatic system -

XX Disclosure: Page 191; 209pp; English.

XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AA194802), a splice variant of human VEGF-3 (AA194806), and
CC nucleic acids encoding them (AAAI5748, AA15762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. Sequences AA15881-AA15895 represent DNA
CC sequences encoding homologues of the human VEGF-3 splice variant from
XX human, mouse and rat.

XX Sequence 389 BP; 89 A; 105 C; 117 G; 78 T; 0 other;

Query Match 69.3%; Score 20.8; DB 21; Length 389;
Best Local Similarity 91.7%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 agcacaagtcgcgatgcagatcc 30
| ||||||| ||||||| ||||||| |||
DB 270 aacacacaagtcgcgatgcagatcc 293

RESULT 20

AAK6306
ID AAK6306 standard; DNA; 2002 BP.
AC AAK6306;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SPQ ID NO:21118.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226881.
PR 22-AUG-2000; 2000US-0226888.
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PR 30-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234474.
PR 25-SEP-2000; 2000US-0234977.
PR 25-SEP-2000; 2000US-0234998.
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PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
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PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 21118; 3071bp + Sequence Listing: English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 2002 BP: 431 A; 506 C; 675 G; 390 T; 0 other;
Query Match 68.7%; Score 20.6; DB 22; Length 2002;
Best Local Similarity 85.2%; Pred. No. 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ggcagcaccgaagtcgagtcgagatcc 30
|||||
Db 1653 ggcagcaccatgctctcatgtgagatcc 1679
RESULT 21
AAK66307
ID AAK66307 standard; DNA: 2205 BP.
XX
AC AAK66307;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21119.
XX
KW Human: immune: haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0224519.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
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PR 08-SEP-2000; 2000US-0232081.
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PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and

PT metastasis -
XX
PS Disclosure; SEQ ID NO 21119; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 2205 BP; 466 A; 582 C; 732 G; 425 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 2205;
Best Local Similarity 85.2%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcagcaccacatccgcgatccagatcc 30
||||||| ||| ||| |||||
Db 1856 ggcagcaccatgctcctcatgagatcc 1882

RESULT 22
AAK6308
ID AAK6308 standard; DNA; 22680 BP.
XX
AC AAK6308;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:21120.
XX
KM Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; OS.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX PA
XX Rosen CA, Barash SC, Ruben SM;
PI WPI: 2001-483426/52.
XX
DR
XX
PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 21120; 3071bp + sequence listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. No. 40;
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RESULT 23

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XX AAK73334;

XX 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO.28146.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

XX WO200157182-A2.

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XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX PS Disclosure; SEQ ID NO 28156; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other:

Query Match          68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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AC
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XX 07-NOV-2001 (first entry)
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XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28437.
DE
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
OS
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XX WO200157182-A2.
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XX 09-AUG-2001.
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XX 17-JAN-2001; 2001WO-US01354.
PF
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XX 31-JAN-2000; 2000US-0179065.
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XX 04-FEB-2000; 2000US-0180628.

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PR 02-OCT-2000; 2000US-0237038.

PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX
XX
XX WPI; 2001-483426/52.
DR
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 28437; 3071bp + Sequence Listing; English.

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33162.
XX
XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
XX WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0232968.
PR 14-SEP-2000; 2000US-0232997.
PR 14-SEP-2000; 2000US-0232998.
PR 14-SEP-2000; 2000US-0232999.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.

PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 33162; 3071pp + Sequence Listing; English.
XX
XX AAK51951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;

Query Match 68.7%; Score 20.6; DB 22; Length 22680;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcgcgatgcagatcc 30
Db 16682 ggcagcaccatgtccatcatgagatcc 16708
|||||

RESULT 29
ABA70982
ID ABA70982 standard; DNA; 197 BP.
XX
AC ABA70982;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #19287.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human foetal liver -
XX
PS Claim 4; SEQ ID NO 19287; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcgcgatgcagatc 29
Db 62 ggcagcaccgaagtcgcgatgcagatc 87
|||||

RESULT 30
ABA37402
ID ABA37402 standard; DNA; 197 BP.
XX
AC ABA37402;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #15868 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -

XX Claim 4; SEQ ID No 15868; 530pp; English.
PS
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcgcgatgcagatc 29
|||||
Db 62 ggcagcaccagtcgcgatgcagatc 87

RESULT 31
AAK19258
ID AAK19258 standard; DNA; 197 BP.
XX
AC AAK19258;
XX
DE 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 19249.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN MO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 19249; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcgcgatgcagatc 29
|||||
Db 62 ggcagcaccagtcgcgatgcagatc 87

RESULT 32
AAK45228
ID AAK45228 standard; DNA; 197 BP.
XX
AC AAK45228;
XX
DE 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 19785.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN MO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 19785; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcgcgatgcagatc 29
|||||
Db 62 ggcagcaccagtcgcgatgcagatc 87

```
RESULT 33
AAI25200
ID AAI25200 standard; DNA; 197 BP.
XX
AC AAI25200;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #15133 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 15133; 487bp; English.
XX
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcggtcgatcgatc 29
   ||||| ||||| ||||| |||||
DB 62 ggcagcaccagtcggtcgatcgatc 87

RESULT 34
AAI51179
ID AAI51179 standard; DNA; 197 BP.
XX
AC AAI51179;
XX
DT 17-OCT-2001 (first entry)
XX
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```
DE Probe #19865 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 19865; 654bp; English.
XX
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 197 BP; 54 A; 45 C; 73 G; 25 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 197;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcggtcgatcgatc 29
   ||||| ||||| ||||| |||||
DB 62 ggcagcaccagtcggtcgatcgatc 87

RESULT 35
ABA58386
ID ABA58386 standard; DNA; 486 BP.
XX
AC ABA58386;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #6691.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
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PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
PS Claim 1; SEQ ID NO 6691; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 486;
Best Local Similarity 84.6%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcggatgcagatc 29
|||||
DB 324 ggcagcaccgaagtcggatgcagatc 349

RESULT 36

ABA27497
ID ABA27497 standard; DNA; 486 BP.
XX
AC ABA27497;
XX
DT 23-JAN-2002 (first entry)
XX

DE Probe #5963 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.

XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.

XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.

XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
XX
PS Claim 1; SEQ ID NO 5963; 530pp; English.
XX
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 486;
Best Local Similarity 84.6%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaagtcggatgcagatc 29
|||||
DB 324 ggcagcaccgaagtcggatgcagatc 349

RESULT 37

AAK06491
ID AAK06491 standard; DNA; 486 BP.
XX
AC AAK06491;
XX
DT 05-NOV-2001 (first entry)
XX

DE Human brain expressed single exon probe SEQ ID NO: 6482.

XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.

XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.

XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX

PS Example 4; SEQ ID NO: 6482; 650pp + Sequence listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.

XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 486;

Best Local Similarity 84.6%; Pred. No. 58;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaagtcgcgagtcagatc 29

Db 324 ggcagaccacgaagcccggtgagctc 349

RESULT 38

AAK32172

ID AAK32172 standard; DNA; 486 BP.

AC AAK32172;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 6729.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukemia; lymphoma; myeloma; ss.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PE 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 6729; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukemia and myeloma. The present sequence is one of

CC the probes of the invention.

XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

OY 4 ggcagaccacgaagtcgcgagtcagatc 29

Db 324 ggcagaccacgaagcccggtgagctc 349

RESULT 39

AAI15983

ID AAI15983 standard; DNA; 486 BP.

AC AAI15983;

DT 12-OCT-2001 (first entry)

DE Probe #5916 for gene expression analysis in human cervical cell sample.

XX Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

XX Homo sapiens.

PN WO200157278-A2.

PD 09-AUG-2001.

PE 30-JAN-2001; 2001WO-US00670.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488901/53.

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human cervical epithelial cells -

XX Claim 25; SEQ ID NO 5916; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes

CC (SENP). The present sequence is one such probe. The SENPs are derived

CC from human HeLa cells. The SENPs can be used to produce a single exon

CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene

CC expression, the probes are therefore useful in grading and/or staging

CC of diseases of the cervix, notably cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 486;

Best Local Similarity 84.6%; Pred. No. 58;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaagtcgcgagtcagatc 29

Db 324 ggcagaccacgaagcccggtgagctc 349

RESULT 40

AAI38021

ID AAI38021 standard; DNA; 486 BP.

AC AAI38021;

```

XX 17-OCT-2001 (first entry)
XX
XX Probe #6707 used to measure gene expression in human placenta sample.
DE
XX
XX Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 6707; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 486 BP; 132 A; 113 C; 151 G; 90 T; 0 other;
SQ
Query Match 65.3%; Score 19.6; DB 22; Length 486;
Best Local Similarity 84.6%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 ggcagcaccgaagtcggatgcagatc 29
Db 324 ggcagcaccgaagtcggatgcagatc 349
RESULT 41
AAV02997/c
ID AAV02997 standard; cDNA; 1956 BP.
XX
XX AAV02997;
AC
XX
XX 06-JUL-1998 (first entry)
XX
XX Murine Ena-VASP like (Evl) cDNA.
DE
XX
XX Ena-VASP like; Evl gene; Mena; mammalian Ena; Enabled;
KW cytoskeleton; cell morphology; cell adhesion; cell motility;
KW cell growth; cell differentiation; ds.
XX
XX Mus musculus.
OS
XX
XX
XX
XX Key Location/Qualifiers
XX CDS 418..1599
XX FT /*tag= a
XX

```

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PN WO9801755-A1.
XX
XX 15-JAN-1998.
XX
XX 03-JUL-1997; 97WO-US11669.
XX
XX 05-JUL-1996; 96US-0675815.
XX
XX (GRFP) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX (HUTC-) HUTCHINSON CANCER RES CENT FRID.
XX
XX Gertler FB, Niebuhr K, Soriano P, Wehland J;
XX
XX WPI; 1998-101197/09.
XX P-PSDB; AAW37149.
XX
XX Detection of modulators of Mena and Ena-VASP-like genes and proteins
XX - used in control of cytoskeletal dynamic events in normal and
XX abnormal cell morphology, adhesion, motility, growth and
XX differentiation
XX
XX Example 1; Page 66-67; 77pp; English.
XX
XX This cDNA comprises murine Ena-VASP like (Evl) cDNA that codes
XX for a 393-amino acid Evl protein (see W37149). It was isolated
XX from a mouse embryonic stem cell cDNA library using human EST
XX clone T80305 as probe; the EST had been identified using a novel
XX mammalian Ena (Mena, see V02996) sequence to search the GenBank
XX database. 2 Novel mammalian genes, Mena and Evl, encoding Mena
XX (see W37148) and Evl are disclosed. Mena and Evl proteins have a
XX discrete, EVH1 functional domain responsible for Mena binding to
XX Listeria, and to the cytoskeletal proteins zyxin and vinculin.
XX Based on the disclosed Mena and Evl genes and proteins, a variety
XX of methods and compositions are provided for screening, isolating
XX and characterizing endogenous and exogenous factors, drugs and
XX therapeutic agents useful to evaluate and/or control cytoskeletal
XX dynamic events involved in normal and abnormal cell morphology,
XX adhesion, motility, growth and/or differentiation. A method of
XX detecting a modulator of Mena activity/expression is claimed.
XX
XX Sequence 1956 BP; 461 A; 571 C; 559 G; 362 T; 3 other;
SQ
Query Match 64.7%; Score 19.4; DB 19; Length 1956;
Best Local Similarity 79.3%; Pred. No. 88;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ctgggcagcaccgaagtcggatgcagatc 29
Db 1092 CAGAGCAGCAGCAGCAGTCGTGATCAGAGC 1064
RESULT 42
AAK70210/c
ID AAK70210 standard; DNA; 7885 BP.
XX
XX AAK70210;
AC
XX
XX 06-NOV-2001 (first entry)
XX
XX Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:25022.
DE
XX
XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytoskeletal; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX

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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225577.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI, 2001-483426/52.
DR
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -


```
CC osteoregulin activity as well as methods of treating mammals for
CC diseases or disorders associated with osteoregulin activity. The
CC modulators of activity may be useful in the manufacture of a
CC medicament for, as well as for treating, a mammal in need of
CC regulation of bone mass and/or density, adiposity, vascular
CC flexibility, and/or atherosclerotic plaque calcification (claimed),
CC for treating and preventing osteoporosis, and for stimulating bone
CC repair and regeneration.
XX
SQ Sequence 1682 BP; 510 A; 401 C; 432 G; 339 T; 0 other;

Query Match      63.3%; Score 19; DB 22; Length 1682;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcaga 27
   ||||| ||||| ||| ||| |||
DB 132 ctgggcagcaccagtcgcgatgcaga 158

RESULT 45
AAQ73500/c
ID AAQ73500 standard; DNA; 8438 BP.
AC AAQ73500;
XX
XX 15-MAY-1995 (first entry)
DE DNA encoding Pseudorabies virus large latency transcript.
XX
XX Pseudorabies virus; PRV; LTV; large latency transcript;
KM attenuated virus; vaccine; early protein 0; EPO; HSV-1 ICP0;
KW protecting animals; deletion mutants; swine; ds.
XX
XX Pseudorabies virus.
OS
FH Key Location/Qualifiers
FT misc_feature 1..7013
   /*tag= a
   /note= "derived from PRV strain Infh"
FT misc_feature 7014..8425
   /*tag= b
   /note= "derived from PRV strain Ka"
FT CDS 622..6498
   /*tag= C
   /note= "encodes predicted amino acid sequence of ORF2"
FT TATA_signal 1..6
   /*tag= d
FT misc_feature 34
   /*tag= e
   /note= "RNA cap site"
FT polyA_signal 8382..8387
   /*tag= f
XX
XX US5352596-A.
XX
XX 04-OCT-1994.
XX
XX 11-SEP-1992; 92US-0945283.
XX
XX 11-SEP-1992; 92US-0945283.
XX
XX (USDA ) US SEC OF AGRIC.
XX
XX Cheung AK, Wesley RD;
XX
XX WPI: 1994-316187/39.
XX
XX P-PSDB; AAR60620.
XX
XX New pseudorabies virus mutants for use in vaccine - having a
XX deletion and/or insertion in the early protein O gene or large
XX latency transcript gene
PT
```

```
XX
PS Disclosure: Column 15-30; 43pp; English.
CC
CC AAQ73500 shows the pseudorabies virus (PRV) large latency transcript
CC (LTV). The basic sequence is derived from PRV strain Infh and PRV
CC strain Ka. The LTV overlaps and is transcribed in the opposite
CC orientation with respect to the EPO (early polypeptide 0) and the
CC immediately early gene (IE180). EPO is nonessential for replicatio,
CC LTR is the only gene expressed during PRV latency, and the IE180
CC gene is absolutely necessary for PRV replication. However there are
CC 2 copies of IE180 in the genome. It is expected that PRV lacking one
CC of the IE180 copies is viable. Deletions in the non-overlapping
CC regions of these 3 genes will generate single deletion mutants,
CC while deletions in overlapping regions will generate double deletion
CC mutants. The invention is concerned with the construction of attenuated
CC viruses which have a reduced ability to reactivate from latency. This
CC can be achieved by functionally disabling the expression of the EPO
CC gene, or by disrupting the synthesis of the LTV, or both. (See also
XX AAQ73501 and AAR60620-24)
XX
SQ Sequence 8438 BP; 1141 A; 2916 C; 3327 G; 1054 T; 0 other;

Query Match      63.3%; Score 19; DB 15; Length 8438;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ggcagcaccagtcgcgatgcagatcc 30
   ||||| ||||| ||| ||| |||
DB 4239 GCCAGCACCAAGTCCGCTCCAGCAC 4213
```

Search completed: September 10, 2002, 01:51:07
Job time: 436 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 00:37:41 : Search time 45.55 seconds
(without alignments)
161.778 Million cell updates/sec.

Title: US-09-912-436-5_COPY_275_304

Perfect score: 30

Sequence: 1 ctgggcagcaccacacgcatcgatgcagatcc 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 99%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.8	89.3	405	1	US-08-469-427A-8
2	26.8	89.3	405	2	US-08-609-443B-8
3	26.8	89.3	405	2	US-08-569-063C-8
4	26.8	89.3	565	1	US-08-469-427A-4
5	26.8	89.3	565	2	US-08-609-443B-4
6	26.8	89.3	565	2	US-08-569-063C-4
7	26.8	89.3	624	2	US-08-609-443B-12
8	26.8	89.3	624	2	US-08-569-063C-12
9	26.8	89.3	886	1	US-08-469-427A-1
10	26.8	89.3	886	2	US-08-609-443B-1
11	26.8	89.3	886	2	US-08-569-063C-1
12	23.6	78.7	591	1	US-08-469-427A-6
13	23.6	78.7	591	2	US-08-609-443B-6
14	23.6	78.7	591	2	US-08-569-063C-6
15	19	63.3	8438	1	US-07-945-283-1
16	18.8	62.7	1748	1	US-08-255-471-8
17	18.4	61.3	81	3	US-08-651-136C-73
18	18.4	61.3	4403765	4	US-09-103-840A-2
19	18.4	61.3	4411529	4	US-09-103-840A-1
20	18	60.0	1096	4	US-08-858-207A-136
21	18	60.0	2210	4	US-08-464-700-53
22	18	60.0	2242	1	US-08-641-627A-37
23	18	60.0	2427	2	US-08-678-039A-39
24	17.8	59.3	1338	2	US-08-044-812A-3
25	17.8	59.3	1338	2	US-08-475-637-3
26	17.8	59.3	1338	3	US-08-706-281A-11
27	17.8	59.3	1338	4	US-09-191-359-3

c	28	17.8	59.3	1338	4	US-09-097-231-11	Sequence 11, Appl
c	29	17.6	58.7	2107	1	US-07-795-859B-3	Sequence 3, Appl1
c	30	17.6	58.7	2107	1	US-08-457-616-3	Sequence 3, Appl1
c	31	17.6	58.7	11873	2	US-08-970-269A-32	Sequence 32, Appl1
c	32	17.6	58.7	11873	2	US-09-407-562-32	Sequence 32, Appl1
c	33	17.6	58.7	11878	2	US-08-970-269A-31	Sequence 31, Appl1
c	34	17.6	58.7	11878	2	US-09-407-562-31	Sequence 31, Appl1
c	35	17.6	58.7	11883	2	US-08-970-269A-28	Sequence 28, Appl1
c	36	17.6	58.7	11883	2	US-09-407-562-28	Sequence 28, Appl1
c	37	17.2	57.3	442	2	US-08-483-528B-53	Sequence 53, Appl1
c	38	17.2	57.3	442	3	US-08-673-799C-53	Sequence 53, Appl1
c	39	17.2	57.3	2599	6	5266464-1	Patent No. 5266464
c	40	17.2	57.3	4330	3	US-09-310-293-1	Sequence 1, Appl1
c	41	17.2	57.3	4330	4	US-09-579-376-1	Sequence 1, Appl1
c	42	17	56.7	1320	2	US-08-641-038A-1	Sequence 1, Appl1
c	43	17	56.7	1320	2	US-09-059-178-1	Sequence 1, Appl1
c	44	17	56.7	1369	2	US-08-642-541-1	Sequence 1, Appl1
c	45	17	56.7	1369	2	US-08-642-541-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-469-427A-8
Sequence 8, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alltalo, Karl
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
TITLE OF INVENTION: DNA CODING THEREFOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-469-427A-8
Query Match 89.3%; Score 26.8; DB 1; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcagatcc 30
||||| ||||||| |||||||
DB 278 CTGGGCAACCAAGTCGAAATGCAGATCC 307

RESULT 2

US-08-609-443B-8
; Sequence 8, Application US/08609443B
; Patent No. 5840693

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-609-443B-8

Query Match 89.3%; Score 26.8; DB 2; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcagatcc 30
||||| ||||||| ||||||| |||||||
DB 278 CTGGGCAACCAAGTCGAAATGCAGATCC 307

RESULT 3
US-08-569-063C-8
; Sequence 8, Application US/08569063C.
; Patent No. 5928939

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-569-063C-8

Query Match 89.3%; Score 26.8; DB 2; Length 405;
Best Local Similarity 93.3%; Pred. No. 0.0081;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcagatcc 30
||||| ||||||| ||||||| |||||||
DB 278 CTGGGCAACCAAGTCGAAATGCAGATCC 307

RESULT 4

US-08-469-427A-4
; Sequence 4, Application US/08469427A
; Patent No. 5607918

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEetical: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-4

Query Match 89.3%; Score 26.8; DB 1; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcgagtcgc 30
||||| ||||||| ||||||| |||||||
Db 273 CTGGGCAACACCAAGTCGATCGAGATCC 302

RESULT 5
US-08-609-443B-4
Sequence 4, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEtical: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-609-443B-4

Query Match 89.3%; Score 26.8; DB 2; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgagtcgagtcgc 30
||||| ||||||| ||||||| |||||||
Db 273 CTGGGCAACACCAAGTCGATCGAGATCC 302

RESULT 6
US-08-569-063C-4
Sequence 4, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
US-08-569-063C-4

Query Match 89.3%; Score 26.8; DB 2; Length 565;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaatcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
DB 273 CTGGGCACACCAAGTCGATGCAGATCC 302

RESULT 7
US-08-609-443B-12
; Sequence 12, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: ALTRALO, Birgitla
; APPLICANT: PAVUSOLA, Kati
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, Mckeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,443B
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
US-08-609-443B-12

Query Match 89.3%; Score 26.8; DB 2; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.0086;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaatcgatgcagatcc 30
||||| ||||||| ||||||| |||||||
DB 275 CTGGGCACACCAAGTCGATGCAGATCC 304

RESULT 8
US-08-569-063C-12
; Sequence 12, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: ALTRALO, Birgitla
; APPLICANT: PAVUSOLA, Kati
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, Mckeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/569,063C
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
US-08-569-063C-12

Query Match 89.3%; Score 26.8; DB 2; Length 624;
Best Local Similarity 93.3%; Pred. No. 0.0086;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccacgaatccgagatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 275 CTGGGCAACACCAAGTCGATCGAGATCC 304

RESULT 9
US-08-469-427A-1
; Sequence 1, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Allitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; IMMEDIATE SOURCE:
; CLONE: pc1f2
; US-08-469-427A-1

Query Match 89.3%; Score 26.8; DB 1; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccacgaatccgagatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 184 CTGGGCAACACCAAGTCGATCGAGATCC 213

RESULT 10
US-08-609-443B-1
; Sequence 1, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta

; APPLICANT: ALLITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; IMMEDIATE SOURCE:
; CLONE: pc1f2
; US-08-609-443B-1

Query Match 89.3%; Score 26.8; DB 2; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccacgaatccgagatgcagatcc 30
||||| ||||||| ||||||| |||||||
Db 184 CTGGGCAACACCAAGTCGATCGAGATCC 213

RESULT 11
US-08-569-063C-1
; Sequence 1, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALLITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: mouse embryo
IMMEDIATE SOURCE:
CLONE: pc1f2
US-08-569-063C-1

Query Match 89.3%; Score 26.8; DB 2; Length 886;
Best Local Similarity 93.3%; Pred. No. 0.009;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| ||||||| ||||||| ||

DB 184 CTGGGCAACACCAAGTCGAGATCGAGATCC 213

RESULT 12
US-08-469-427A-6
Sequence 6, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-6

Query Match 78.7%; Score 23.6; DB 1; Length 591;
Best Local Similarity 86.7%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctgggcagcaccagtcgcgatgcagatcc 30
||||| ||||||| ||||||| ||||||| ||

DB 278 CTGGGCAACACCAAGTCGAGATCGAGTAC 307

RESULT 13
US-08-609-443B-6
Sequence 6, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-609-443b-6

Query Match 78.7%; Score 23.6; DB 2; Length 591;
Best Local Similarity 86.7%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaatccgatgcagatcc 30
||||| ||||||| ||||||| |||
Db 278 CTGGGCAACACCAAGTCGATCGAGGTAC 307

RESULT 14
US-08-569-063c-6
Sequence 6, Application US/08569063c
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Karl
APPLICANT: PAUSOLA, Karl
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063c
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 591 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-569-063c-6

Query Match 78.7%; Score 23.6; DB 2; Length 591;
Best Local Similarity 86.7%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctgggcagcaccgaatccgatgcagatcc 30
||||| ||||||| ||||||| |||
Db 278 CTGGGCAACACCAAGTCGATCGAGGTAC 307

RESULT 15
US-07-945-283-1/c
Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The EP0 and LIT Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
STATE: IL
COUNTRY: USA
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4128
TELEFAX: 309-685-4011 ext.513
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudorabies virus
FEATURE:
NAME/KEY: CDS
LOCATION: 622..6495
FEATURE:
NAME/KEY: variation
LOCATION: replace(1099, "g")
FEATURE:
NAME/KEY: variation
LOCATION: replace(1267, "t")
FEATURE:

APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 61.3%; Score 18.4; DB 4; Length 4403765;
Best Local Similarity 78.6%; Pred. No. 48;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ttggcagaccagtcgagtcgagtc 29
Db 77236 ttggcagaccagtcgagtcgagtc 77263

RESULT 19
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 61.3%; Score 18.4; DB 4; Length 4411529;
Best Local Similarity 78.6%; Pred. No. 48;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ttggcagaccagtcgagtcgagtc 29
Db 77257 ttggcagaccagtcgagtcgagtc 77284

RESULT 20
US-08-858-207A-136
Sequence 136, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard

APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smlnkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSP for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-136

Query Match 60.0%; Score 18; DB 4; Length 1096;
Best Local Similarity 80.8%; Pred. No. 50;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ttggcagaccagtcgagtcgagtc 27
Db 1021 TTGGCTGCACCAATCCTGTTCACA 1046

RESULT 21
US-08-464-700-53/C
Sequence 53, Application US/08464700
Patent No. 6232458
GENERAL INFORMATION:
APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN L
TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,700
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435

```

1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: AU PL6520
3      FILING DATE: 22-DEC-1992
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER: AU PL9661
6      FILING DATE: 28-JUN-1993
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: PCT/AU93/006555
9      FILING DATE: 16-DEC-1993
10     ATTORNEY/AGENT INFORMATION:
11     NAME: Bak, Mary E.
12     REGISTRATION NUMBER: 31,215
13     REFERENCE/DOCKET NUMBER: GRC303A
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: 215-540-9200
16     TELEFAX: 215-540-5818
17     INFORMATION FOR SEQ ID NO: 53:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 2210 base pairs
20     TYPE: nucleic acid
21     STRANDEDNESS: double
22     TOPOLOGY: linear
23     MOLECULE TYPE: cDNA
24     HYPOTHEetical: NO
25     ANTI-SENSE: NO
26     OS-08-464-700-53

```

Query Match	60.0%	Score 18;	DB 4;	Length 2210;
Best Local Similarity	80.8%	Pred. NO. 55;		
Matches 21; Conservative	0;	Mismatches	5;	Indels 0;
				Gaps 0

Qy	4	g	c	a	c	c	a	a	a	g	t	c	c	g	a	t	c	a	t	c	29
Db	1577	G	C	C	A	C	C	A	A	G	C	C	C	A	G	C	T	G	C	A	1552

RESULT 22
 US-08-641-627A-37/C
 Sequence 37 Application US/08641627A
 Patent No. 5726040
 GENERAL INFORMATION:
 APPLICANT: Ensley Phd, Burt D.
 APPLICANT: Ludmer, Matthew
 TITLE OF INVENTION: Cosmetic Compositions Including
 TITLE OF INVENTION: Tropoelastin Isomorphs
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Choate, Hall & Stewart
 STREET: 53 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: usa
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/641,627A
 FILING DATE: 02-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jarrell Ph.D., Brenda H.
 REGISTRATION NUMBER: 39,223
 REFERENCE/DOCKET NUMBER: 0062912-0001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-5000
 TELEFAX: (617) 248-4000
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2242 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; STRAIN: tropoelastin CDNA (CHE-3)
US-08-641-627A-37

```

Query Match	60.0%;	Score 18;	DB 1;	Length 2242;
Best Local Similarity	80.8%;	Pred. No. 55;		
Matches 21;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0

QY	4	g	c	a	c	c	a	a	a	g	t	c	c	g	a	t	c	a	g	a	t	c		29
Db	1714	G	C	C	A	C	C	A	A	G	C	C	C	A	G	C	T	G	C	A	G	C	T	1689

```

RESULT 23
US-08-678-039A-39/C
: Sequence 39, Application US/08678039A
: Patent No. 5858662
: GENERAL INFORMATION:
: APPLICANT: Keating, Mark T.
: APPLICANT: Morris, Colleen A.
: TITLE OF INVENTION: Diagnosis of Williams Syndrome and
: TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
: TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Rothwell, Piggy, Ernst & Kurz, P.C.
: STREET: 555 Thirteenth Street, N.W., Suite 701 East
: STREET: Tower
: City: Washington
: STATE: DC
: COUNTRY: U.S.A.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/678,039A
: FILING DATE: 10-JUL-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Saxe, Stephen A.
: REGISTRATION NUMBER: 36,609
: REFERENCE/DOCKET NUMBER: 2323-120A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-624-1589
: TELEFAX: 202-783-6031
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2427 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 49..2424
: US-08-678-039A-39

```


OY 4 ggcagcaccagtcgcgagtcagatc 29
| | | | | | | | | | | | | | | | |
DB 1800 GCCAGCACCAGCCGCGCTGCAGCTC 1775

RESULT 24
US-08-044-812A-3/C

; Sequence 3, Application US/08044812A

; Patent No. 5837521

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; APPLICANT: Roselli-Rehuss, Linda

; APPLICANT: Mountjoy, Kathleen G

; APPLICANT: Robbins, Linda S

; TITLE OF INVENTION: Mammalian Melanocyte Stimulating Hormone

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/044,812A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5837521nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 92,835

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 910-221-5317

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1338 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..297

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 298..1269

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: 1270..1338

; US-08-044-812A-3

Query Match 59.3%; Score 17.8; DB 2; Length 1338;

Best Local Similarity 75.9%; Pred. No. 62;

Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 tgggcagcaccagtcgcgagtcgagatc 30
| | | | | | | | | | | | | | | | |
DB 292 TCGGCGGAGCAGTTCGCGCTGCAGCTCC 264

RESULT 25

US-08-475-637-3/C

; Sequence 3, Application US/08475637

; Patent No. 5994087

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; APPLICANT: Roselli-Rehuss, Linda

; APPLICANT: Mountjoy, Kathleen G

; APPLICANT: Robbins, Linda S

; TITLE OF INVENTION: Mammalian Melanocyte Stimulating Hormone

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,637

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/044,812

; FILING DATE: 04-APR-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5994087nan, Kevin E

; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 92,835

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; TELEX: 910-221-5317

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1338 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..297

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 298..1269

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: 1270..1338

; US-08-475-637-3

Query Match 59.3%; Score 17.8; DB 2; Length 1338;

Best Local Similarity 75.9%; Pred. No. 62;

Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 tgggcagcaccagtcgcgagtcgagatc 30
| | | | | | | | | | | | | | | | |
DB 292 TCGGCGGAGCAGTTCGCGCTGCAGCTCC 264

RESULT 26

US-08-706-281A-11/C

; Sequence 11, Application US/08706281A

; Patent No. 6100048

; GENERAL INFORMATION:

; APPLICANT: Cone, Roger D

; APPLICANT: Fan, Wei

; APPLICANT: Boston, Bruce A

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..297
FEATURE:
NAME/KEY: CDS
LOCATION: 298..1269
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1270..1338
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-097-231-11

Query Match 59.3%; Score 17.8; DB 4; Length 1338;
Best Local Similarity 75.9%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 ttggcagaccacgaagtcggatgcagatcc 30
||||| ||||| ||||| ||||| |||||
Db 292 TCGCGGGGACCAAGTTCGGGCTGCAGATCC 264

RESULT 29
US-07-795-859B-3/C
Sequence 3, Application US/07795859B
Patent No. 5422262
GENERAL INFORMATION:
APPLICANT: Anderson, Stefan
APPLICANT: Russell, David W.
TITLE OF INVENTION: Steroid 5'-Reductases
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P O Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/795,859B
FILING DATE: 18-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:260/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7677
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 31..807
US-07-795-859B-3

Query Match 58.7%; Score 17.6; DB 1; Length 2107;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctggcagaccacgaagtcggatgc 24
||||| ||||| ||||| ||||| |||||
Db 1430 CTGGCTGGAACAGTCCAGATGC 1407

RESULT 30
US-08-457-616-3/C
Sequence 3, Application US/08457616
Patent No. 5679521
GENERAL INFORMATION:
APPLICANT: Anderson, Stefan
APPLICANT: Russell, David W.
TITLE OF INVENTION: Steroid 5'-Reductases
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P O Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,616
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/795,859
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:260/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7677
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 31..807
US-08-457-616-3


```

; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970_269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11878 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
;
US-08-970-269A-31

Query Match          58.7%; Score 17.6; DB 2; Length 11878;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 gcagaccacgaatcgatgcagat 28
        ||||| ||||| ||||| |||||
Db      5519 GCAGACGACGAGTGGGATTCAGAT 5542

RESULT 34
US-09-407-562-31
; Sequence 31, Application US/09407562
; Patent No. 6294334
; GENERAL INFORMATION:
; APPLICANT: Katheryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,562
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/970,269
; FILING DATE: No. 6294334ember 14, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 31:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11878 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; FEATURE:
;
US-09-407-562-31

Query Match          58.7%; Score 17.6; DB 4; Length 11878;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 gcagaccacgaatcgatgcagat 28
        ||||| ||||| ||||| |||||
Db      5519 GCAGACGACGAGTGGGATTCAGAT 5542

RESULT 35
US-08-970-269A-28
; Sequence 28, Application US/08970269A
; Patent No. 5976803
; GENERAL INFORMATION:
; APPLICANT: Katheryn Meek
; TITLE OF INVENTION: Genetic Test For Equine Severe
; TITLE OF INVENTION: Combined Immunodeficiency Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,269A
; FILING DATE: No. 5976803ember 14, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler Ph.D., Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5860
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11883 bp
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
;
US-08-970-269A-28

Query Match          58.7%; Score 17.6; DB 2; Length 11883;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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OY 5 gcagcaccgaatccgagatgcagat 28
||||| ||||| ||||| |||||
DB 5521 GCAGCAGCAAGTGGGATTCAGAT 5544

RESULT 36
US-09-407-562-28

; Sequence 28, Application US/09407562
; Patent No. 6294334

; GENERAL INFORMATION:

; APPLICANT: Kathryn Meek

; TITLE OF INVENTION: Genetic Test For Equine Severe

; TITLE OF INVENTION: Combined Immunodeficiency Disease

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dr. Benjamin A. Adler

; STREET: 8011 Candle Lane

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Macintosh

; SOFTWARE: Microsoft Word for Macintosh

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/407,562

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/970,269

; FILING DATE: No. 6294334ember 14, 1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Adler Ph.D., Benjamin A.

; REGISTRATION NUMBER: 35,423

; REFERENCE/DOCKET NUMBER: D5860

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-777-2321

; TELEFAX: 713-777-6908

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11883 bp

; TYPE: nucleic acid

; STRANDEDNESS: double stranded

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: other nucleic acid

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; US-09-407-562-28

; Query Match 58.7%; Score 17.6; DB 4; Length 11883;

; Best Local Similarity 83.3%; Pred. No. 1e+02;

; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 gcagcaccgaatccgagatgcagat 28
||||| ||||| ||||| |||||

DB 5521 GCAGCAGCAAGTGGGATTCAGAT 5544

RESULT 37

US-08-483-528B-53

; Sequence 53, Application US/08483528B

; Patent No. 5939532

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: KUMANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHAYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,528B

; FILING DATE: 07-JUN-95

; CLASSIFICATION: 536

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4100

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 442 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "synthetic DNA"

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens and mouse

; FEATURE:

; NAME/KEY: sig-peptide

; LOCATION: -19..-1

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; FEATURE:

; NAME/KEY: domain

; LOCATION: 31..35

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; OTHER INFORMATION: /product= "CDR1"

; FEATURE:

; NAME/KEY: domain

; LOCATION: 50..66

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; OTHER INFORMATION: /product= "CDR2"

; FEATURE:

; NAME/KEY: domain

; LOCATION: 99..109

; IDENTIFICATION METHOD: by similarity with known sequence or to an established

; OTHER INFORMATION: /product= "CDR3"

; US-08-483-528B-53

; Query Match 57.3%; Score 17.2; DB 2; Length 442;

; Best Local Similarity 73.3%; Pred. No. 95;

; Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ctgggcagcaccgaatccgagatgcagatc 30
||| | ||||| ||||| |||||

DB 124 CTGACCTGCACCGTGTCCGGATACACATTC 153

RESULT 38

US-08-673-799C-53

; Sequence 53, Application US/08673799C

; Patent No. 6042828

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: KOIKE, MASAMICHI

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

APPLICANT: KUMANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,799C
FILING DATE: 27-JUN-96
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
ORIGINAL SOURCE:
ORGANISM: Homo sapiens and mouse
FEATURE:
NAME/KEY: sig-peptide
LOCATION: -19...-1
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
FEATURE:
NAME/KEY: domain
LOCATION: 31...35
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
OTHER INFORMATION: /product= "CDR1"
FEATURE:
NAME/KEY: domain
LOCATION: 50...66
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
OTHER INFORMATION: /product= "CDR2"
FEATURE:
NAME/KEY: domain
LOCATION: 99...109
IDENTIFICATION METHOD: by similarity with known sequence or to an established cc
OTHER INFORMATION: /product= "CDR3"
US-08-673-799C-53
Query Match 57.3%; Score 17.2; DB 3; Length 442;
Best Local Similarity 73.3%; Pred. No. 95;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ctggcgacgacccaagtcggatgcagatcc 30
||| | |||| | |||| | ||| |
Db 124 ctgacctgcacccgtgtccgatatcacatttc 153
RESULT 39
5266464-1
; Patent No. 5266464
; APPLICANT: HOUSEY, GERRARD
; TITLE OF INVENTION: METHOD OF SCREENING FOR PROTEIN INHIBITORS
; AND ACTIVATORS
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,073

FILING DATE: 10-AUG-16989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 154,206
FILING DATE: 10-FEB-1988
SEQ ID NO:1:
LENGTH: 2599
5266464-1
Query Match 57.3%; Score 17.2; DB 6; Length 2599;
Best Local Similarity 73.3%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ctggcgacgacccaagtcggatgcagatcc 30
||| | ||| | ||| | ||| | ||| |
Db 1281 ctgggaagcccccattccctgactcagatcc 1310
RESULT 40
US-09-310-293-1
; Sequence 1, Application US/09310293
; Patent No. 6117662
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard L.
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Traini, Christopher M.
; APPLICANT: Mathie, Thomas B.
; TITLE OF INVENTION: Respiratory nitrate reductase alpha
; FILE REFERENCE: GM10000
; CURRENT APPLICATION NUMBER: US/09/310,293
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/086,579
; EARLIER FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4330
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-310-293-1
Query Match 57.3%; Score 17.2; DB 3; Length 4330;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ctggcgacgacccaagtcggatgcagatcc 30
||| | |||| | |||| | ||| |
Db 1328 ctggctagcaccgaatccgtgtccagatgc 1357
RESULT 41
US-09-579-376-1
; Sequence 1, Application US/09579376
; Patent No. 6316237
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard L.
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Traini, Christopher M.
; APPLICANT: Mathie, Thomas B.
; TITLE OF INVENTION: Respiratory nitrate reductase alpha
; FILE REFERENCE: GM10000
; CURRENT APPLICATION NUMBER: US/09/579,376
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/310,293
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/086,579
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

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; LENGTH: 4330
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-579-376-1

```

Query Match	57.38;	Score 17.2;	DB 4;	Length 4330;
Best Local Similarity	73.38;	Pred. No. 1.3e+02;		
Matches 22;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;

OY	1	ctggcgacgacccaagtccgcatgtcagatcc	30
Db	1328	ctggtcagcaccgcgaatccctggttcagatgc	1357

RESULT 42
US-08-641-038A-1
; Sequence 1, Application US/08641038A

GENERAL INFORMATION:
APPLICANT: SODA, KENJI
APPLICANT: TANAKA, HIDEHIKO
APPLICANT: INOUE, HIROYUKI
APPLICANT: INAGAKI, KENJI
APPLICANT: ESAKI, NOBUYOSHI
TITLE OF INVENTION: RECOMBINANT L-METHIONINE GAMMA-LYASE

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH

COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE

```
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30
```

APPLICATION NUMBER: US/08/641,038A
FILING DATE:

CLASSIFICATION: 455
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0020-3989
TELECOMMUNICATION INFORMATION:

```

1      TELEPHONE: (703) 205-8000
2      TELEFAX: (703) 205-8050
3
4      INFORMATION FOR SEQ ID NO: 1:
5
6          SEQUENCE CHARACTERISTICS:
7
8              LENGTH: 1320 base pairs
9              TYPE: nucleic acid
10             STRANDEDNESS: double
11             TOPOLOGY: linear
12
13             MOLECULE TYPE: other nucleic acid
14
15             FEATURE:

```

```

; NAME/KEY: CDS
; LOCATION: 61..1254
US-08-641-038A-1

```

Query Match	56.7%	Score 17	DB 2	Length 1320
Local Similarity	80.0%	Pred. No. 1.4e+02		
Matches 20, Conservative	0	Mismatches 5	Indels 0	Gaps 0

QY 1 ctggcgagcaccgaagtcgcatgca 25
 ||||| |||| | |||| ||||
 Db 385 CTGGGCAACACCCCTGTACGGCTGCA 409

RESULT 43

US-09-059-178-1
; Sequence 1, Application US/09059178
; Patent No. 5863788
; GENERAL INFORMATION:

APPLICANT: INOUE, HIROYUKI
APPLICANT: INAGAKI, KENJI
APPLICANT: ESAKI, NOBUYOSHI
STREET OR TERRACE DOORWAY AND METEOROLOGICAL STATION

```

; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; DO NOT SAY

```

STATE: VA
COUNTRY: USA
ZIP: 22040-0747

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APPLICATION NUMBER: 08/641,038
FILING DATE:
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0020-3989
TELECOMMUNICATION INFORMATION:

```

; TELEFAX: (703) 205-8050
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```

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;
; TYPE: nucleic acid
; STRANDEDNESS: double
;

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;
; TOPOLOGY: linear
;
; MOLECULE TYPE: other nucleic acid
;
FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: 61..1254
;
US-09-059-178-1

```

Query Match	56.7%	Score 17	DB 2	Length 1320
Best Local Similarity	80.0%	Pred. No. 1.4e+02		
Matches 20; Conservative	0	Mismatches 5	Indels 0	Gaps 0

0y 1 ctgycagcaccacgtccgcatgca 25
||||| ||| ||| |||
Db 385 CTGGGCAACACCCCTGTACGGCTGCA 409

RESULT 44
US-08-642-541-1
; Sequence 1, Application US/08642541

APPLICANT: YUYING, TAN
TITLE OF INVENTION: HIGH EXPRESSION MODULES ENCODING
TITLE OF INVENTION: METHIONINASE, PURIFIED RECOMBINANT METHIONINASE PRODUCED

```

; TITLE OF INVENTION: THEREFROM AND USES THEREOF
;
; NUMBER OF SEQUENCES: 8
;
; CORRESPONDENCE ADDRESS:
;

```

```

; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington

```


STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,541
FILING DATE: 03-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Millman, Robert A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 31276-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1241
US-08-642-541-1

Query Match 56.7%; Score 17; DB 2; Length 1369;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatga 25
||||| ||||| ||||| |||||
DB 372 CTGGCACAACCTGTACGCTGCA 396

RESULT 45
US-08-642-541-3/C
Sequence 3, Application US/08642541
Patent No. 5891704
GENERAL INFORMATION:
APPLICANT: YUYING, TAN
TITLE OF INVENTION: HIGH EXPRESSION MODULES ENCODING
TITLE OF INVENTION: METHIONINASE, PURIFIED RECOMBINANT METHIONINASE PRODUCED
NUMBER OF INVENTIONS: THEREFROM AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,541
FILING DATE: 03-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Millman, Robert A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 31276-20002.21
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-642-541-3

Query Match 56.7%; Score 17; DB 2; Length 1369;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcggatga 25
||||| ||||| ||||| |||||
DB 998 CTGGCACAACCTGTACGCTGCA 974

Search completed: September 10, 2002, 01:51:28
Job time: 4427 sec

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Result No.	Score	Query Match	Length	DB	ID	Description
1	28.4	94.7	405	9	AA784595	AA784595 zb63h10.g
2	28.4	94.7	935	9	AL529876	AL529876 AL529876
3	27.4	91.3	699	10	BE297480	BE297480 60117604.r
4	26.8	90.0	531	9	AA434485	AA434485 zw3ia04.r
5	26.8	89.3	799	10	BF582738	BF582738 602094155B
6	26.8	89.3	919	10	BM007641	BM007641 603617063
7	26	86.7	445	9	AA292448	AA292448 zt29f01.r
8	26	86.7	685	10	BI823209	BI823209 603039477
9	23.6	78.7	266	9	BB374531	BB374531 BB374531
c 10	23.6	78.7	555	12	AE341037	AE341037 1M0073815
11	22.2	74.0	423	9	AA073660	AA073660 mm94a06.r
12	21	70.0	579	10	BI082710	BI082710 602850965
13	20.8	69.3	389	9	AI174183	AI174183 uc07b07.r
14	20.6	68.7	620	10	BE243867	BE243867 601070480
15	20.6	68.7	714	10	BF688367	BF688367 602185443
16	20.6	68.7	783	10	BE254933	BE254933 601114886
17	20.6	68.7	793	10	BE547100	BE547100 601072507

18	20.6	68.7	828	10	BF345759	BF345759	602017820
19	20.6	68.7	1131	10	BF984155	BF984155	602306859
20	20.6	68.0	565	12	A206632	RCCT-23-3	A206632
21	20.4	68.0	851	10	BM008260	BM008260	603616890
22	20	66.7	336	9	AM828906	r47c11.y	AM828906
23	20	66.7	369	9	AA594466	AA594466	tl194d03.s
24	20	66.7	407	10	BE578204	BE578204	tl90d07.y
25	20	66.7	437	9	AM828935	AM828935	r48c04.y
26	20	66.7	492	9	AJ283475	AJ283475	4A3B-AAC-
27	20	66.7	530	10	BG364270	BG364270	d91g07.y
28	20	66.7	530	10	BJ096360	BJ096360	BJ096360
29	20	66.7	536	9	AM828856	AM828856	r46a03.y
30	20	66.7	547	10	BJ038957	BJ038957	BJ038957
31	20	66.7	563	10	BG170692	BG170692	ps11n.pk0
32	20	66.7	572	10	BJ035192	BJ035192	BJ035192
33	20	66.7	579	10	BJ094267	BJ094267	BJ094267
34	20	66.7	653	9	AV871222	AV871222	AV871222
35	20	66.7	658	9	AM642247	AM642247	cm17e04.w
36	20	66.7	663	10	BJ093942	BJ093942	BJ093942
37	20	66.7	677	10	BG037489	dc51h04.y	BG037489
38	20	66.7	691	9	AL593991	AL593991	AL593991
39	20	66.7	716	10	BJ013567	BJ013567	BJ013567
40	20	66.7	1014	9	AL518419	AL518419	AL518419
41	20	66.7	1040	12	CNS03KIE	AL248207	Tetraodon
42	19.6	65.3	99	9	AA738943	AA738943	v68d06.r
43	19.6	65.3	499	12	BH389734	BH389734	AG-ND-125
44	19.6	65.3	794	10	BM007748	BM007748	603616745
45	19.6	65.3	878	12	CNS037B8	AL231101	Tetraodon

ALIGNMENTS

RESULT	1
LOCUS	AM784595
DEFINITION	405 bp mRNA linear EST 19-MAY-2000 zb63hl0.91 Canis cDNAs from mdck cells Canis familiaris CDNA clone zb63hl0.5', mRNA sequence.
ACCESSION	AM784595
VERSION	AM784595.1 GI:7838908
KEYWORDS	EST.
SOURCE	dog.
ORGANISM	Canis familiaris
REFERENCE	Eukaryota; Metazoa; Chordata; Carnivora; Fissipedia; Canidae; Canis. Mammalia; Eutheria; Caniyoza; Fissipedia; Canidae; Canis. 1 (bases 1 to 405)
AUTHORS	Mccomble,W.R., See,L.-H., Baker,J.P., Bahret,A., Dedhia,N.N., de la Bastide,M., Huang,E.N., King,L., Kirchoff,K.A., Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R., Rodriguez,M.A., Shah,R.S., Shekher,M., Spiegel,L.A., Toth,K., Vill.M.D. and Hannon ,G.J.
TITLE	Expressed sequence tags from Canis familiaris (dog)
JOURNAL	Unpublished (2000)
COMMENT	Contact: W. Richard McComble Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcomble@cshl.org Plate: zb63 row: h column: 10 Seq primer: -40M13revUniv High quality sequence stop: 405. Location/Qualifiers 1..405 /organism="Canis familiaris" /db_xref="taxon:9615" /clone="zb63hl0" /clone_lib="Canis cDNAs from mdck cells" /note="Vector: lambda Zap II; The library was provided by Greg Hannon (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from exponentially growing mdck
FEATURES	
SOURCE	

cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT 65 a 138 c 132 g 68 t 2 others

ORIGIN

Query Match 94.7%; Score 28.4; DB 9; Length 405;
Best Local Similarity 96.7%; Pred. No. 1;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgatcgatcc 30
|||||
DB 329 CTGGGCAGCACCAGTCCGATGCAGATCC 358

RESULT 2
LOCUS AL529876 935 bp mRNA linear EST 13-FEB-2001
DEFINITION AL529876 LTI_NFL001.NBC4 Homo sapiens cDNA clone CS0DD005YH10 5
prime, mRNA sequence.
ACCESSION AL529876
VERSION AL529876.1 GI:12793369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 935)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers

1..935
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD005YH10"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 182 a 319 c 287 g 141 t 6 others
ORIGIN

Query Match 94.7%; Score 28.4; DB 9; Length 935;
Best Local Similarity 96.7%; Pred. No. 1.1;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgatcgatcc 30
|||||
DB 413 CTGGGCAGCACCAGTCCGATGCAGATCC 442

RESULT 3
LOCUS BE297480 699 bp mRNA linear EST 20-JUL-2000
DEFINITION 601176041F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531179 5',
mRNA sequence.
ACCESSION BE297480

VERSION BE297480.1 GI:9181160
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 699)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10CM205 row: b column: 12
High quality sequence start: 35
High quality sequence stop: 657.

FEATURES
Location/Qualifiers

1..699
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3531179"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOT8; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 130 a 247 c 201 g 121 t
ORIGIN

Query Match 91.3%; Score 27.4; DB 10; Length 699;
Best Local Similarity 96.6%; Pred. No. 2.5;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgatcgatcc 29
|||||
DB 202 CTGGGCAGCACCAGTCCGATGCAGACC 230

RESULT 4
LOCUS AA434485 531 bp mRNA linear EST 29-MAY-1997
DEFINITION zw31a04.r1 Soares ovary tumor NBH07 Homo sapiens cDNA clone
IMAGE:770862 5', similar to TR:G1216398 G1216398 VEGF RELATED FACTOR
ISOFORM VRF167 PRECURSOR. ;, mRNA sequence.

ACCESSION AA434485
VERSION AA434485.1 GI:2139399
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 531)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Maita, M., Martin, O., Moore, B.,
, Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
, T., Waterston, R., and Wilson, R.

TITLE Mashu-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LINTL; contact the
IMAGE Consortium (info@image.lnlnl.gov) for further information
Seq primer: 28m13 rev2 Et from Amersham
High quality sequence stop: 470.

FEATURES

Source

```

/organism="Homo sapiens"
/db_xref="DB:5980735"
/db_xref="taxon:9606"
/clone IMAGE:770862"
/clone_1b="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT73p (pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5
TGTTACCAATCTGTAAGTCGAGCGCCGCGTCTTTTCTTTTCTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaído."

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Query Match	90.0%;	Score 27;	DB 9;	Length 531;
Best Local Similarity	100.0%;	Pred. No. 3.4;		
Matches 27; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Oy	4	ggcagcaccacgaftccgatgcagatcc	30
Db	191	GGCAGCACCAAGTCGCGATGCAGATCC	217

RESULT	5				
BF582738					
LOCUS	BF582738	799 bp	mRNA	linear	EST 12-DEC-2000
DEFINITION	60209615881 NCI-CGAP-Co24 Mus musculus CDNA clone IMAGE:4208222 5',				
	mRNA sequence.				

ACCESSION	BF582738	GI:11656456
VERSION	BF582738.1	
KEYWORDS	EST.	

SOURCE ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus
1 (pages 1 to 799)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LAM9772 row: d column: 15
High quality sequence stop: 711.
Location/Qualifiers

Sol

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/organism="Mus musculus"  
/strain="FVB/N"  
/db_xref="taxon:10090"  
/clone="IMAGE:4208222"  
/clone_lib="NCI_CGAP_Co24"
```

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/ab_host="DH10B (T1 phage-resistant)"
/lot="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dr
Average insert size 1.6 kb Constructed by life
Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT      210 a      203 g      145 t
ORIGIN
      241 c

```

BASE COUNT
ORIGIN

Query Match	89.3%;	Score 26.8;	DB 10;	Length 799;
Best Local Similarity	93.3%;	Pred. No. 4.2;		
Matches 28; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	ctggcgagcaccgaagtccggtatgcagatcc	30
Db	61	CTGGCAACACCAGTCCGATGCAGATCC	90

RESULT	6				
	BM007641				
LOCUS	BM007641	919 bp	mRNA	linear	EST 30-OCT-2001
DEFINITION	603617063p1 NIH_MGC_113		Homo sapiens	CDNA clone IMAGE:5441079 5'	
	mRNA sequence.				

ACCESSION	BM00/641	GI:16521995
VERSION	BM007641.1	
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM

REFERENCE	
AUTHORS	NIH-MGC http://mgc.nhl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: L1CML1914 row: m column: 16
High quality sequence stop: 669.

FEATURES

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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:5441079"
/clone_1ib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notice="Organ: spleen; Vector: pORF1; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT      179 a      230 c      328 g      182 t
ORIGIN

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Query Match	89.3%;	Score 26.8;	DB 10;	Length 919;
Best Local Similarity	93.3%;	Pred. No. 4.3;		
Matches	28;	Conservative	0;	Mismatches 2;
				Indels 0;
				Gaps 0

[illegible]

[illegible]

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 685)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LRAM11449 row: P column: 17 High quality sequence stop: 402. Location/Qualifiers 1..685 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5180416" /clone_lib="NIH_MGC_115" /lab_host="DH10B" /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."
BASE COUNT	182 a 232 c 178 g 93 t
ORIGIN	
Query Match	86.7%; Score 26; DB 10; Length 685;
Best Local Similarity	100.0%; Pred. NO. 8.2;
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
Db	1 GCAGCACCACAGTCGGATGCAGATCC 26
Qy	5 gcagcaccacagtcggatgcagatcc 30
RESULT	9
BB374531	
LOCUS	BB374531 266 bp mRNA linear EST 13-JUL-2000
DEFINITION	BB374531 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130075112 3' similar to AF032925 Rattus norvegicus vascular endothelial growth factor B 186 precursor, mRNA sequence.
ACCESSION	BB374531
VERSION	BB374531.1 GI:9087025
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hitozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata Y., Shimemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya

LOCUS	AA073660	423 bp	mRNA		linear	EST 15-FEB-1997
DEFINITION	mm4g5966.r1 Striatogene mouse heart (#937316)	Mus musculus cDNA clone IMAGE:536122 5' similar to TR:G1314336 G1314336 MVRP167.				; , mRNA sequence.
ACCESSION	AA073660					
VERSION	AA073660.1	GI:1595394				
KEYWORDS	EST.					
SOURCE	house mouse,					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	(bases 1 to 423) Marra, S., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T., Schellander, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.					
TITLE	The WashU-HHMI Mouse EST Project					
JOURNAL	Unpublished (1996)					
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through INLNL ; contact the IMAGE Consortium (info@image.inl.gov) for further information. MGI:323058 Seq primer: -28m13 rev1 ER from Amersham High quality sequence stop: 411. Location/Qualifiers					
FEATURES	Source					
	1..423					
	/organism="Mus musculus"					
	/strain="NIH/Swis"					
	/db_xref="taxon:10090"					
	/clone="IMAGE:536122"					
	/clone_lib="Striatogene mouse heart (#937316)"					
	/sex="pooled"					
	/tissue_type="heart"					
	/dev_stage="13 day embryos"					
	/lab_host="SOLR (kanamycin resistant)"					
	/note="Organ: heart; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 93 pooled NIH/Swis 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCGAG 3' -3' adaptor sequence: 5' CTCGACTTTTTTTTTTTTTTTTT 3'"					
BASE COUNT	96 a 135 c 123 g 69 t					
ORIGIN						
Query Match	74.0%; Score 22.2; DB 9;					
Best Local Similarity	88.9%; Pred. NO.1.9e+02;					
Matches 24:	Conservative 0; Mismatches 3; Indels 0; Gaps 0;					
OY	4 gccagcaccacaagtccgatgcagatcc 30					
DB	52 gcgaacaccagaatcgcaatgcagatcc 78					
RESULT 12						
B1087310	B1087310	579 bp	mRNA		linear	EST 20-JUN-2001
LOCUS	602850965r1 NIH_MGC_10 Homo sapiens CDNA clone IMAGE:4992305 5'					
DEFINITION	mRNA sequence.					
ACCESSION	B1087310					
VERSION	B1087310.1	GI:14505640				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					

REFERENCE	1 (bases 1 to 579)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@b3-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LHAM1011 row: b column: 18 High quality sequence stop: 579. Location/Qualifiers
FEATURES	1..579
source	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4992305" /clone_id="NIH_MGC_10" /cell_line="MGC36" /lab_host="DH10B" /note="Organ: Cervix; Vector: PCMV-SPOrt6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT	123 a 211 c 154 g 91 t
ORIGIN	
Query Match	70.0%; Score 21; DB 10; Length 579;
Best Local Similarity	100.0%; Prid. No. 5,4e+02;
Matches 21; Conservativity	0; Mismatches 0; Indels 0; Gaps 0;
Oy	10 accaaagtcggatgcagatcc 30
Db	22 ACCAAGTCGGATGCAGATCC 42
RESULT 13	
LOCUS	A1174183 389 bp mRNA linear EST 07-OCT-1998
DEFINITION	uc07b07.t1 Soares_mammary_gland.NbMKG Mus musculus cDNA clone IMAGE:1397269 5' similar to SW:VGBB_MOUSE_P49766 VASCULAR ENDOTHelial GROWTh FACTOR B PRECURSOR ;, mRNA sequence.
ACCESSION	A1174183
VERSION	A1174183.1 GI:3720325
KEYWORDS	EST.
SOURCE	house mouse. Mus musculus.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 389) Marra,M., Hillier,D., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
AUTHORS	The WashU-HIMI Mouse EST Project Unpublished (1996)
TITLE	Contact: Marra M/Mouse EST Project
JOURNAL	WashU-HIMI Mouse EST Project
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. NCI:908985 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 378.


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FEATURES
source
    Location/Qualifiers
        1..389
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone_lib="IMAGE:1397269"
        /sex="male"
        /tissue_type="mammary_gland_NbMMG"
        /dev_stage="4 weeks"
        /lab_host="DH10B"
        /note="Organ: mammary gland; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACCAATCTGACAGTGGAGCGCCGCAATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      89 a      105 c      117 g      78 t
ORIGIN

Query Match
Best Local Similarity  69.3%; Score 20.8; DB 9; Length 389;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 agcaccaagtcgagtcgagatcc 30
Db 270 AACACCAAGTCCGATGCAGATCC 293

RESULT 14
BE543967
LOCUS
DEFINITION BE543967 620 bp mRNA linear EST 09-AUG-2000
601070480F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456642 5',
mRNA sequence.
ACCESSION BE543967
VERSION BE543967.1 GI:9772612
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 620)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM8444 row: P column: 19
High quality sequence stop: 620.
Location/Qualifiers
    1..620
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="IMAGE:3456642"
    /clone_1lb="NIH_MGC_12"
    /tissue_type="cervical carcinoma cell line"
    /lab_host="DH10B"
    /note="Organ: cervix; Vector: PCMV-SF0RT6; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.4 kb. Library prepared by Life

BASE COUNT      130 a      250 c      213 g      121 t
ORIGIN

Query Match
Best Local Similarity  68.7%; Score 20.6; DB 10; Length 714;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcacacccaagtcgagtcgagatcc 30
Db 221 GGCACACCAATGCTCTCATGGAGATCC 247

RESULT 16
BE254933
LOCUS
DEFINITION BE254933 783 bp mRNA linear EST 13-JUL-2000
602185443F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:429658 5',
mRNA sequence.
ACCESSION BE688367
VERSION BE688367.1 GI:11973775
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 714)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LUCM1157 row: f column: 11
High quality sequence stop: 701.
Location/Qualifiers
    1..714
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="IMAGE:429658"
    /clone_1lb="NIH_MGC_43"
    /tissue_type="normal pigmented retinal epithelium"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
    EcoRI; cDNA made by oligo-dT priming, directionally
    cloned into EcoRI/XhoI sites using the following 5'
    adaptor: GGCACGAG(G). Library constructed by Ling Hong
    in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC Library. I"

BASE COUNT      130 a      250 c      213 g      121 t
ORIGIN

Query Match
Best Local Similarity  85.2%; Pred. No. 7.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ggcacacccaagtcgagtcgagatcc 30
Db 221 GGCACACCAATGCTCTCATGGAGATCC 247
```

DEFINITION 60111886F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352484 5', mRNA sequence.

ACCESSION BE254933

VERSION BE254933.1 GI:9125366

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 783)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: L1CM151 row: 1 column: 21

High quality sequence stop: 665.

Location/Qualifiers

1..783

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3352484"

/clone_1lb="NIH_MGC_16"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 125 a 273 c 242 g 143 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 783;

Best Local Similarity 85.2%; Pred. No. 7.9e+02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaatcgatgcagatcc 30

Db 341 ggcagaccacgaatcgatgcagatcc 367

RESULT 17

BE547100 793 bp mRNA linear EST 09-AUG-2000

LOCUS 601072507F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458856 5', mRNA sequence.

ACCESSION BE547100

VERSION BE547100.1 GI:9775665

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 793)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: L1AM8450 row: m column: 01

High quality sequence stop: 639.

Location/Qualifiers

1..793

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3458856"

/clone_1lb="NIH_MGC_12"

/tissue_type="cervical carcinoma cell line"

/lab_host="DH10B"

/note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

BASE COUNT 139 a 273 c 239 g 142 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 793;

Best Local Similarity 85.2%; Pred. No. 7.9e+02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagaccacgaatcgatgcagatcc 30

Db 152 ggcagaccacgaatcgatgcagatcc 178

RESULT 18

BF345759 828 bp mRNA linear EST 22-NOV-2000

LOCUS 602017820F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153397 5', mRNA sequence.

ACCESSION BF345759

VERSION BF345759.1 GI:11293354

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 828)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: L1AM9421 row: h column: 06

High quality sequence stop: 766.

Location/Qualifiers

1..828

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4153397"

/clone_1lb="NCI_CGAP_Brn67"

/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 147 a 266 c 265 g 150 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 828;
 Best Local Similarity 85.2%; Pred. No. 8e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaatcgcgatcgatcc 30
 ||||||| |||| |||| |||||
 Db 473 GGCAGCACCATGCTCTCATGAGATCC 499

RESULT 19
 BF984155 1131 bp mRNA linear EST 23-JAN-2001
 DEFINITION 602306859F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4397966 5',
 mRNA sequence.
 ACCESSION BF984155 GI:12386967
 VERSION BF984155
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1131)
 NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM10099 row: f column: 15
 High quality sequence stop: 720.

FEATURES
 source Location/Qualifiers
 1..1131
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4397966"
 /clone_1lb="NIH-MGC_88"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: small intestine; Vector: PCMV-SPORT6;
 Site.1: NotI; Site.2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 265 a 358 c 318 g 190 t
 ORIGIN

Query Match 68.7%; Score 20.6; DB 10; Length 1131;
 Best Local Similarity 85.2%; Pred. No. 8.3e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccgaatcgcgatcgatcc 30
 ||||||| |||| |||| |||||
 Db 378 GGCAGCACCATGCTCTCATGAGATCC 404

RESULT 20
 A2026632 565 bp DNA linear GSS 25-FEB-2000
 DEFINITION RPCI-23-345P3.J1 RPCI-23 Mus musculus genomic clone RPCI-23-345P3,
 DNA sequence.
 ACCESSION A2026632
 VERSION A2026632.1 GI:7102016
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS Zhao, S., Nieman, W., Feldblyum, T., Malek, V., Shatsman, S., Akintet
 , B., Levins, M., McGann, S., Teegye, G., Geer, K., Kroll, M., de Jong, P.
 and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other_GSSs: RPCI-23-345P3.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (inforesgen.com). BAC end page:
http://www.tigr.org/tdb/bac.ends/mouse/bac_end_intro.html
 Plate: 345 row: P column: 3
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..565
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-345P3"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site.1:
 EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Site
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 120 a 149 c 180 g 115 t
 ORIGIN

Query Match 68.0%; Score 20.4; DB 12; Length 565;
 Best Local Similarity 80.0%; Pred. No. 9e+02;
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ctggagcagcaccgaatcgcgatcgatcc 30
 ||||||| |||| |||| |||||
 Db 369 CTGGGACAGCACCAAGCAGCTGCTGAGAGAC 340

RESULT 21
 BM008260 851 bp mRNA linear EST 30-OCT-2001
 LOCUS BM008260
 DEFINITION 603616890F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440486 5',
 mRNA sequence.
 ACCESSION BM008260
 VERSION BM008260
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 851)
 NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-f@mail.nih.gov

Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM1913 row: d column: 23
 High quality sequence stop: 699.

FEATURES

source

Location/Qualifiers

1..851

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5440486"

/clone_1lb="NIH.MGC.113"

/lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; CDNA made by oligo-dt priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH.MGC Library."

BASE COUNT

233 a 219 c 244 g 154 t 1 others

ORIGIN

Query Match

Best Local Similarity 68.0%; Score 20.4; DB 10; Length 851;

Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ctggagcagcagcagtcgagtcagatcc 30

Db 537 CTGGCAGCAGCAGGTTCACATGCAGTCCC 508

RESULT 22

AM829906/c

LOCUS

DEFINITION ra47c11.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita

CDNA 5', mRNA sequence.

AM829906.1 GI:7923720

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..336

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1058309"

/clone_1lb="NCI-CGAP_Co10"

/tissue_type="colon tumor RER"

/lab_host="DH10B"

/note="Organ: colon; Vector: pRT3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

RER+ colon tumor, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified pRT73

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo (N-Soares4)."

BASE COUNT

68 a 98 c 112 g 91 t

ORIGIN

source

1..336

/organism="Meloidogyne incognita"

/db_xref="taxon:6306"

/clone_1lb="Bird-Rao Meloidogyne incognita J2"

/dev_stage="enriched for 2nd stage juveniles"

/lab_host="X10RL"

/note="Vector: ZAP express - pBCKMV (Stratagene); Site_1:

EcoRI; Site_2: XhoI; Oligo (dT) primed library. CDNA was

constructed and cloned unidirectionally into the vector

within the 5' EcoRI and 3' XhoI sites. This library was

constructed by Dr. Uma Rao and Dr. David Bird at North

Carolina state University."

BASE COUNT 114 a 50 c 60 g 112 t

ORIGIN

Query Match

Best Local Similarity 66.7%; Score 20; DB 9; Length 336;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 gggcagcagcagtcgagtcgagtcagatcc 30

Db 214 GGGCAGCTCCAGTCCGCTGTCGCC 187

RESULT 23

AA594466

LOCUS

DEFINITION n194d03.s1 NCI-CGAP_Co10 Homo sapiens CDNA clone IMAGE:1058309 3',

mRNA sequence.

AA594466.1 GI:2409816

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..369

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1058309"

/clone_1lb="NCI-CGAP_Co10"

/tissue_type="colon tumor RER"

/lab_host="DH10B"

/note="Organ: colon; Vector: pRT3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

RER+ colon tumor, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified pRT73

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo (N-Soares4)."

BASE COUNT

68 a 98 c 112 g 91 t

ORIGIN

Query Match	66.7%	Score 20;	DB 10;	Length 369;
Best Local Similarity	82.1%	Pred. No. 1.2e+03;		
Matches 23; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;
3	gggcagcaccacgacgcatgcagatcc 30			
Db 135	GGGCGCCCACTAAGTCGGGACGACATCC 162			

RESULT 24	
BE578204/c	
LOCUS	
DEFINITION	BE578204 407 bp mRNA linear EST 10-MAY-2001
ACCESSION	FK09B07.y1 Meloidogyne javanica Egg SL1 Topol Kloeck Chiapelli
VERSION	McCarter Meloidogyne javanica cDNA 5', mRNA sequence.
KEYWORDS	BE578204.1 GI:9829146
SOURCE	EST.
ORGANISM	root-knot nematode.
REFERENCE	Meloidogyne javanica
AUTHORS	Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
TITLE	1 (bases 1 to 407)
JOURNAL	McCarter, J., Clifton, S., Chiapelli, B., Page, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, T., Gibbons, M., Rittler, E., Bennett, J., Franklin, C., Tsagaris, H., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, R., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., Mcann, R., Waterston, R. and Wilson, R.
COMMENT	The Washington Univ. Nematode EST Project, 1999
	Unpublished (1999)
	Contact: McCarter JP
	The Washington Univ. Nematode EST Project, 1999
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@watson.wustl.edu
	The library was constructed by Dr. Andrew Kloeck
	(kloeck@biology.wustl.edu) at Divergence LLC, and Brandi Chiapelli
	(bchiapelle@watson.wustl.edu) and Dr. Jim McCarter
	(jmcarter@watson.wustl.edu) at Washington University Genome
	Sequencing Center. DNA Sequencing by: Washington University Genome
	Sequencing Center St. Louis.
	Seq primer: -40RP from Gibco.
FEATURES	Location/Qualifiers
SOURCE	1..407
	/organism="Meloidogyne javanica"
	/db_xref="taxon:6303"
	/clone_lib="Meloidogyne javanica Egg SL1 Topol Kloeck
	Chiapelli McCarter"
	/dev_stage="enriched for eggs"
	/lab_host="DH10B"
	/note="Vector: pCRII-TOPO; SL1-Oligo(dT) PCR-based
	library. Meloidogyne javanica cDNA PCR products of size
	approximately 600-1200 nucleotides containing SL1 on the
	5' end and oligo(dT) on the 3' end were non-directionally
	cloned into pCRII-TOPO (Invitrogen) following the Topo TA
	cloning protocol. cDNA products were size separated. The
	cDNA insert can be excised by digestion with EcoRI. The
	library was constructed by Dr. Andrew Kloeck at Divergence
	LLC and Brandi Chiapelli and Dr. James McCarter at
	Washington University, St. Louis. Nematodes were provided
	by Dr. David Bird of North Carolina State University."
BASE COUNT	148 a 62 c 66 g 131 t
ORIGIN	

Query Match	66.7%	Score 20;	DB 10;	Length 407;
Best Local Similarity	82.1%	Pred. No. 1.2e+03;		
Matches 23; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;
23; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

RESULT 25	AM829955	437 bp	mRNA	linear	EST 10-MAY-2001
LOCUS	ra8bc04.y1	Bird-Rao	Meloidogyne incognita J2	Meloidogyne incognita	
DEFINITION	cDNA 5', mRNA sequence.				
ACCESSION	AM829955				
VERSION	AM829955.1	GI:7923770			
KEYWORDS	EST.				
SOURCE	southern root-knot nematode.				
ORGANISM	Meloidogyne incognita				
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.				
AUTHORS	1 (bases 1 to 437) McCarter,J., Clifton,S., Chipelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Thelsing,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisbill,R., Ronko,I., Kennedy,S., Maguire,J., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.				
TITLE	The Washington Univ. Nematode EST Project, 1999				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu The library was constructed by Uma Rao and David Bird (david.bird@mcu.edu) at North Carolina State University. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Seq primer: -40RP from Gibco.				
FEATURES	Location/Qualifiers				
source	1..437 /organism="Meloidogyne incognita" /db_xref="taxon:6306" /clone_lib="Bird-Rao Meloidogyne incognita J2" /dev_stage="enriched for 2nd stage juveniles" /lab_host="XtLR0L" /note="Vector: ZAP express - pBKCMV (Stratagene); Site_1: EcoRI; Site_2: XhoI; Oligo (dtd) primed library. cDNA was constructed and cloned unidirectionally into the vector within the 5' EcoRI and 3' XhoI sites. This library was constructed by Dr. Uma Rao and Dr. David Bird at North Carolina State University."				
BASE COUNT	162 a 63 c 71 g 141 t				
ORIGIN					
Query Match	66.7%	Score 20;	DB 9;	Length 437;	
Best Local Similarity	82.1%	Pred. NO. 1.2e+03;			
Matches 23;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;	
QY	3 gggcagcaccaagtcgcatgcagatcc 30 				
DB	214 GGGCAGCTCCAGTCGCGCTGCTGGGCC 187				
RESULT 26	AJ283475	492 bp	mRNA	linear	EST 30-JUN-2000
LOCUS	AJ283475/c				
DEFINITION	4A3B-AAC-B-03-F Anopheles gambiae immune competent 4A3B Anopheles gambiae cDNA clone 4A3B-AAC-B-03, mRNA sequence.				
ACCESSION	AJ283475				
VERSION	AJ283475.1	GI:6931354			

KEYWORDS	EST.
SOURCE	African malaria mosquito.
ORGANISM	Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea ; Anophelinae. 1 (bases 1 to 492)
REFERENCE	Dimopoulos G., Casavant, T. L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J.J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C. Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000) 2030950
AUTHORS	Contact: Dimopoulos G Fotis C. Kafatos Laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany.
COMMENT	Location/Qualifiers 1..492
FEATURES	/organism="Anopheles gambiae" /strain="4A i/r" /db_xref="taxon:7165" /clone="4A3B-AAC-B-03" /cell_line="Anopheles gambiae immune competent 4A3B" /lab_host="E. coli DH10B" /note="Vector: pYT73D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from the forward priming site that reads from the 3' end of cDNA. The 4A3B is a directionally cloned and normalized cDNA library that was constructed from the 4A3B cell line o1igo-T primed cDNA according to: Bonaldo, Lennon & Soares (1986): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
BASE COUNT	87 a 155 c 157 g 93 t
ORIGIN	
Query Match	66.7%; Score 20; DB 9; Length 492;
Best Local Similarity	82.1%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY 3	ggcgagccgaatgcggaatgcagatcc 30
Db 196	CGCCGCGCACGCAGTCGGTTCAGATGC 169
RESULT 27	
BG364270/c	530 bp linear EST 08-MAR-2001
LOCUS	dc91q07.y1 NICHD XCC O01 xenopus laevis cDNA clone IMAGE:3404724 5'
DEFINITION	similar to TR:Q9V812 Q9V812 CG6550 PROTEIN.; mRNA sequence.
ACCESSION	BG364270
VERSION	BG364270.1 GI:13253367
KEYWORDS	EST.
SOURCE	African clawed frog.
ORGANISM	Xenopus laevis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 530) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. dna11.cgap@femail.nih.gov Tissue Procurement: Martha Rabbett, Steven L. Klein, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU) DNA Sequencing by: Washington University Sequencing Center
JOURNAL	
COMMENT	

FEATURES	source	location/Qualifiers
1..530	/organism="Xenopus laevis"	
	/db_xref="taxon:8355"	
	/clone="IMAGE:3404724"	
	/clone_lib="NICHD XGC 001"	
	/tissue_type="Oocytes"	
	/lab_host="DH10B (phage-resistant)"	
	/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."	
BASE COUNT	171 a 113 c 131 g 114 t	1 others
ORIGIN		
Query Match	66.7%; Score 20; DB 10; Length 530;	
Best Local Similarity	82.1%; Pred. No. 1.3e+03;	
Matches 23; Conservative	0; Mismatches 5; Indels 0; Gaps 0;	
Oy	2	tgggcagcagcaagtcgcgagtcagcagtc 29
Db	326	TGAGCAGCCCCCATGTACGATCCAGATC 299
RESULT 28		
BU096360/c		530 bp mRNA linear EST 12-DEC-2001
LOCUS	BU096360	NIBB Mochli normalized Xenopus early gastrula library
DEFINITION	Xenopus laevis cDNA clone XL153k16 5', mRNA sequence.	
ACCESSION	BU096360	
VERSION	BU096360.1	GI:17597244
KEYWORDS	EST.	
SOURCE	African clawed frog.	
ORGANISM	Xenopus laevis	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;	
	Xenopodinae; Xenopus.	
	1 (bases 1 to 530)	
REFERENCE	Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara	
AUTHORS	Y.	
TITLE	Expressed genes in X. laevis embryo	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Tadasu Shin-i	
	Center For Genetic Resource Information	
	National Institute of Genetics	
	1111 Yata, Mishima, Shizuoka 411-8540, Japan	
	Tel: 81-559-81-6856	
	Fax: 81-559-81-6855	
	Email: tshini@genes.nig.ac.jp.	
FEATURES		
source		Location/Qualifiers
	1..530	
	/organism="Xenopus laevis"	
	/db_xref="taxon:8355"	
	/clone="XL153k16"	
	/clone_lib="NIBB Mochli normalized Xenopus early gastrula	
	library"	
	/tissue_type="whole embryo"	
	/dev_stage="stage 10.5"	
BASE COUNT	173 a 118 c 128 g 110 t	1 others
ORIGIN		
Query Match	66.7%; Score 20; DB 10; Length 530;	
Best Local Similarity	82.1%; Pred. No. 1.3e+03;	
Matches 23; Conservative	0; Mismatches 5; Indels 0; Gaps 0;	
Oy	2	tgggcagcagcaagtcgcgagtcagcagtc 29
Db	260	TGAGCAGCCCCCATGTACGATCCAGATC 233

RESULT 29
 AM828856/c 536 bp mRNA linear EST 10-MAY-2001
 LOCUS ra69a03.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
 DEFINITION CDNA 5' similar to WP:C36E6.B CE20542 ;, mRNA sequence.
 ACCESSION AM828856
 VERSION AM828856.1 GI:7922655
 KEYWORDS EST.
 SOURCE southern root-knot nematode.
 ORGANISM Meloidogyne incognita
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
 REFERENCE 1 (bases 1 to 536)
 McCarter,J., Clifton,S., Chapell,I., B., Pape,D., Martin,J., Wylie,T.,
 Dente,M., Marita,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
 Gibbons,M., Rittler,E., Bennett,D., Franklin,C., Tsagaris,I., R.,
 Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepien,
 M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
 Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
 Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Uma Rao and David Bird
 (david_bird@esu.edu) at North Carolina State University. DNA
 Sequencing by: Washington University Genome Sequencing Center St.
 Louis.
 Seq primer: -40RP from GIBCO
 High quality sequence stop: 444.
 Location/Qualifiers
 source 1..536
 /organism="Meloidogyne incognita"
 /db_xref="taxon:6306"
 /clone_lib="Bird-Rao Meloidogyne incognita J2"
 /dev_stage="enriched for 2nd stage juveniles"
 /lab_host="XLOL1"
 /note="Vector: ZAP express - PBKCMV (Stratagene). Site 1:
 EcoRI; Site 2: XhoI; Oligo (dT) primed library. CDNA was
 constructed and cloned unidirectionally into the vector
 within the 5' EcoRI and 3' XhoI sites. This library was
 constructed by Dr. Uma Rao and Dr. David Bird at North
 Carolina state University."
 BASE COUNT 211 a 73 c 91 g 161 t
 ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 536;
 Best Local Similarity 82.1%; Pred. No. 1.3e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 gggcagcaccagtcgcatcgatccagatcc 30
 ||||| ||||| ||||| ||||| |||||
 Db 214 GGGCAGCTCCAGTCCGGCTGCTGCGCC 187

RESULT 30
 BU038957 547 bp mRNA linear EST 07-DEC-2001
 LOCUS BU038957/c
 DEFINITION laevis CDNA clone X1045p19 5', mRNA sequence.
 ACCESSION BU038957
 VERSION BU038957.1 GI:17408453
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis

REFERENCE
 AUTHORS Kityama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasi Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 source 1..547
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_lib="X1045p19"
 /clone_lib="NIBB Mochii normalized Xenopus neurula
 library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 BASE COUNT 182 a 118 c 132 g 115 t
 ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 547;
 Best Local Similarity 82.1%; Pred. No. 1.3e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 tggcagcaccagtcgcatcgatccagatc 29
 || ||||| || || ||||| |||||
 Db 260 TGAGCAGCCCCCATGTACGATCCAGATC 233

RESULT 31
 BG710692 563 bp mRNA linear EST 08-MAY-2001
 LOCUS BG710692
 DEFINITION pgl.in.pk004.k8 Normalized liver library Gallus gallus CDNA clone
 pgl.in.pk004.k8 5' similar to pIRIS15904|s15904 alpha-1 proteinase
 inhibitor III, variant 1 precursor - rat emb|CA37176.1| (X52984)
 alpha(10-inhibitor 3, precursor [Rattus norvegicus]G, mRNA
 sequence.
 BG710692
 ACCESSION BG710692.1 GI:14004642
 VERSION BG710692
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 563)
 AUTHORS Burnside,J., Morgan,R.W. and Cogburn,L.A.
 TITLE Chicken ESTs from a normalized liver library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joan Burnside
 Molecular Endocrinology
 University of Delaware
 40 Townsend Hall, Newark, DE 19717, USA
 Tel: 302 831-1345
 Fax: 302-831-3411
 Email: joan@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers
 source 1..563
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone_lib="pgl.in.pk004.k8"
 /clone_lib="Normalized Liver Library"
 /sex="Male and Female"
 /tissue_type="liver"
 /lab_host="E.coli EMDH108"

BASE COUNT 117 a /note=Vector: pckvSPORT 6"
159 c 184 g 103 t
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 563;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 9ggcagcaccagtcgcgatgcagatcc 30
1 ||||| |||| |||| ||||| ||
Db 362 GAGCAGACGACGACCGCTGCAGAGCC 389

RESULT 32 572 bp mRNA linear EST 07-DEC-2001
BJ035192/c
LOCUS BJ035192 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL021e08 5', mRNA sequence.
ACCESSION BJ035192
VERSION BJ035192.1 GI:17414445
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
SOURCE Location/Qualifiers
1..572
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL021e08"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"

BASE COUNT 181 a 121 c 146 g 124 t
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 572;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 2 1gggagcagcaccagtcgcgatgcagatc 29
1 ||||| |||| |||| ||||| |||||
Db 369 TGAGCAGCCCGCTGTCGATCCAGATC 342

RESULT 33 579 bp mRNA linear EST 12-DEC-2001
BJ094267/c
LOCUS BJ094267 NIBB Mochii normalized Xenopus early gastrula library
DEFINITION Xenopus laevis cDNA clone XL144p09 5', mRNA sequence.
ACCESSION BJ094267
VERSION BJ094267.1 GI:17594218
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

Xenopodinae; Xenopus.
1 (bases 1 to 579)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.

JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
SOURCE Location/Qualifiers
1..579
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL144p09"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
library"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"

BASE COUNT 193 a 121 c 145 g 120 t
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 579;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 1gggagcagcaccagtcgcgatgcagatc 29
1 ||||| |||| |||| ||||| |||||
Db 294 TGAGCAGCCCGCTGTCGATCCAGATC 267

RESULT 34 653 bp mRNA linear EST 08-NOV-2001
AV871222/c
LOCUS AV871222 Nori Satoh unpublished cDNA library, egg Clona
DEFINITION intestinalis cDNA clone r1eg26f08 3', mRNA sequence.
ACCESSION AV871222
VERSION AV871222.1 GI:16858746
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Clona.
1 (bases 1 to 653)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.

JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
SOURCE Location/Qualifiers
1..653
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="r1eg26f08"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"

BASE COUNT 153 a 140 c 146 g 211 t 3 others
ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 653;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

JOURNAL
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: rcs@dcps.femail.nih.gov
Tissue Procurement: Martha Rehbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 407.
Location/Qualifiers
1. .677
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3400926"
/clone_lib="NICHD XGC Emb3"
/tissue_type="embryo (stages 24-25)"
/lab_host="DH10B (phage-resistant)"
/note="Vector: PCMV-SPORE6; Site 1: NotI; Site 2: SalI;
Cloned unidirectional. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."

BASE COUNT 217 a 135 c 168 g 157 t
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 677;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 tgggcagcaccagtcgcgagtcagatc 29
|| ||||| ||| || ||||| |||||
Db 335 TGACGAGCCCATGTACGATCCAGATC 308

RESULT 38
AL593991/c 691 bp mRNA linear EST 30-JUN-2001
LOCUS AL593991 XGC-gastrula Silurana tropicalis cDNA clone Tgas004k14 5',
DEFINITION mRNA sequence.
ACCESSION AL593991
VERSION AL593991.1 GI:15006052
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 691)
Huckle, E., Taylor, R., McMurray, A., Ashurst, J. L., Zorn, A. M. and
Rogers, J.
REFERENCE Sanger Xenopus tropicalis EST project 2001
AUTHORS Sanger Xenopus tropicalis EST project 2001
TITLE Unpublished (2001)
JOURNAL Contact: Huckle E
COMMENT Sanger Centre
Hinnton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tgas004k14.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
location/Qualifiers
1. .691
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Tgas004k14"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA

was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into PCS107 with EcoRI at the 5' end and NotI at the 3'
end."

BASE COUNT 229 a 146 c 173 g 143 t
ORIGIN

Query Match 66.7%; Score 20; DB 9; Length 691;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 tgggcagcaccagtcgcgagtcagatc 29
|| ||||| ||| || ||||| |||||
Db 245 TGACGAGCCCATGTACGATCCAGATC 218

RESULT 39
BU013567 716 bp mRNA linear EST 05-DEC-2001
LOCUS BU013567 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA190G08 5',
DEFINITION mRNA sequence.
ACCESSION BU013567
VERSION BU013567.1 GI:17363442
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 716)
Kohara, Y., Shin-I, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
REFERENCE Medaka EST project in Takeda's lab
AUTHORS Unpublished (2001)
TITLE Contact: Tadasu Shin-I
JOURNAL Center for Genetic Resource Information
COMMENT National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin1@genes.nig.ac.jp.
location/Qualifiers
1. .716
/organism="Oryzias latipes"
/strain="Hd-R"
/db_xref="taxon:8090"
/clone="MF01SSA190G08"
/clone_lib="MF01SSA cDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
BASE COUNT 184 a 193 c 144 g 194 t 1 others
ORIGIN

Query Match 66.7%; Score 20; DB 10; Length 716;
Best Local Similarity 82.1%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctgggcagcaccagtcgcgagtcagatc 28
|| ||||| ||||| ||| ||||| |||||
Db 172 CTGGGAGACACACCTCTCTGTCAGAGT 199

RESULT 40
AL518419 1014 bp mRNA linear EST 13-FEB-2001
LOCUS AL518419 IRT_NFI011 NRC1 Homo sapiens cDNA clone CS0DA009YM24 3
DEFINITION prime, mRNA sequence.
ACCESSION AL518419
VERSION AL518419.1 GI:12781912
KEYWORDS EST.

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 1014)
TITLE	Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
FEATURES	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: secre@genoscope.cns.fr , Web : www.genoscope.cns.fr .
SOURCE	location/Qualifiers
	1..1014
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="CS0DA009YM24"
	/clone_11b="TRI_NFL011_NBC1"
	/sex="male"
	/tissue_type="neuroblastoma cells"
	/lab_host="DH10B"
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com "
BASE COUNT	169 a 336 c 270 g 231 t 8 others
ORIGIN	
Query Match	66.7%; Score 20; DB 9; Length 1014;
Best Local Similarity	82.1%; Pred. No. 1.4e+03;
Matches	23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy	3 gggcagaccacgaatccgagtcgacgtcc 30
Db	85 GGGCGCCACACAGTCGGGACGACGATCC 112
RESULT 41	
CNS03KIE	
LOCUS	CNS03KIE 1040 bp DNA linear GSS 17-MAY-2000
DEFINITION	Tetradodon nigroviridis genome survey sequence PUC-Orl end of clone 033J11 of library G from Tetradodon nigroviridis, genomic survey sequence.
ACCESSION	AL248207.1 GI:7969219
VERSION	AL248207
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetradodon nigroviridis.
ORGANISM	Tetradodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorpha; Tetradontiformes; Tetradontidae; Tetradodon.
REFERENCE	1 (bases 1 to 1040)
AUTHORS	Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bonnaeu,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1040)
AUTHORS	Roest-Crollius,H., Jalllon,O., Dasilva,C., Bonnaeu,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Human gene number estimate provided by genome wide analysis using Tetradodon nigroviridis DNA sequence

```

JOURNAL      Unpublished
REFERENCE    3 (bases 1 to 1040)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT      This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/tetraodon.
FEATURES
    source
        1..1040
            /organism="Tetraodon nigroviridis"
            /db_xref="taxon:99883"
            /clone="03Jf11"
            /clone_11b="G"
            /note="Genoscope sequence ID : COBG033CE06Sp1-end :
            PUC-Or1"
BASE COUNT   201 a      346 c      270 g      219 t      4 others
ORIGIN
Query Match      66.7% Score 20; DB 12; Length 1040;
Best Local Similarity 82.1%; Pred. 1.4e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY      3 gggcagacccaagtcgagatcgatcc 30
          1 1111 11111111 1111 111
AA738943/c      99 bp      mRNA      linear      EST 14-JAN-1998
LOCUS          AA738943/c
DEFINITION     vvf68d06.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
                IMAGE:1227563 5' similar to gb:X01697 Mouse mRNA fragment for
                parotid secretory protein (MOUSE);, mRNA sequence.
ACCESSION      AA738943
VERSION        AA738943.1 GI:27761195
KEYWORDS       EST.
SOURCE         house mouse.
ORGANISM       Mus musculus.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 99)
AUTHORS        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
                Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                Waterston,R.
                The WashU-HHMI Mouse EST Project
                Unpublished (1996)
                Contact: Marra M/Mouse EST Project
                WashU-HHMI Mouse EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel.: 314 286 1800
                Fax: 314 286 1810
                Email: mouseest@watson.wustl.edu
                This clone is available royalty-free through LNL; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                MGI:653155
                Trace considered overall poor quality
                Seq primer: -28m13 rev1 EF from Amersham
                High quality sequence stop: 1.
FEATURES
    source
        1..99
            /organism="Mus musculus"
            /strain="C57BL/6"
            /db_xref="taxon:10090"
            /clone="IMAGE:1227563"
            /clone_11b="Stratagene mouse skin (#937313)"
            /sex="females"
            /tissue_type="whole skin"

```

/dev-stage="11 weeks old"
/lab-host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site: 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGACGACGAC 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 27 a 17 c 28 g 27 t
ORIGIN

Query Match 65.3%; Score 19.6; DB 9; Length 99;
Best Local Similarity 84.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ggcagcaccagtcgcgagtcagatcc 30
||||| ||||| ||||| ||||| |||||
Db 48 GCAGAACCAAGTCACATCCAGATCC 23

RESULT 43
BH389734 499 bp DNA linear GSS 11-DEC-2001
LOCUS AG-ND-12512.TR ND-TAM Anopheles gambiae genomic clone AG-ND-12512,
DEFINITION DNA sequence.
ACCESSION BH389734
VERSION BH389734.1 GI:17335875
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae
; Anophelinae.

REFERENCE 1 (bases 1 to 499)
AUTHORS Shetty J., Malek J., Koo H., Collins F., Gardner M. and Loftus B.J.
TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: AG-ND-12512.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest
Seq primer: M13 Rev
Class: BAC ends.

FEATURES
source Location/Qualifiers

1..499
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-12512"
/clone_11b="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT 171 a 98 c 77 g 153 t
ORIGIN

Query Match 65.3%; Score 19.6; DB 12; Length 499;
Best Local Similarity 84.6%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ggcagcaccagtcgcgagtcagatcc 30
||||| || ||||| ||||| ||||| |||||
Db 156 GCAGACGACACCTCGGATCGATCGATCC 131

RESULT 44
BM007478 794 bp mRNA linear EST 30-OCT-2001
LOCUS 603616745F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440619 5',
DEFINITION mRNA sequence.
ACCESSION BM007478
VERSION BM007478.1 GI:16521832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 794)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgep@s-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: L10C1913 row: 1 column: 12
High quality sequence start: 7
High quality sequence stop: 397.
Location/Qualifiers

FEATURES
source

1..794
/organism="Homo sapiens"
/db_xref="taxon:3606"
/clone="IMAGE:5440619"
/clone_11b="NIH_MGC_113"
/lab-host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pORF7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAGGAG(g). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 168 a 209 c 240 g 176 t 1 others
ORIGIN

Query Match 65.3%; Score 19.6; DB 10; Length 794;
Best Local Similarity 84.6%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ggcagcaccagtcgcgagtcagatcc 29
||||| ||||| ||||| ||||| |||||
Db 182 GCCAGCACCACCAAGCCAGATCGACGCTC 157

RESULT 45
CNS037B8 878 bp DNA linear GSS 15-MAY-2000
LOCUS CNS037B8
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
001F16 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL231101
VERSION AL231101.1 GI:7890096
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Tetradon nigroviridis
Tetradon nigroviridis

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS
1 (bases 1 to 878)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 878)
Roest-Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE
JOURNAL
REFERENCE
AUTHORS
3 (bases 1 to 878)
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

COMMENT
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
1..878
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="001F16"
/clone.lib="G"
/note="Genoscope sequence ID : COBG001DC08LPI-end : T7"
location/Qualifiers

BASE COUNT
ORIGIN
186 a 242 c 274 g 159 t 17 others

Query Match 65.3%; Score 19.6; DB 12; Length 878;
Best Local Similarity 84.6%; Pred. No. 1.9e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ctgggcagcaccaagtcgagatgcag 26
| ||||| ||| ||||| |||
Db 461 CGGGGACGCCGACGTCGGATGGAG 486

Search completed: September 10, 2002, 01:12:19
Job time: 5851 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 01:47:27 ; Search time 61.65 Seconds
(without alignments)
245.029 Million cell updates/sec

Title: US-09-912-436-6

Perfect score: 719
Sequence: 1 MSPLLRLALLALQLAPAQ.....EHSQCRCRPPKKDSAVKPD 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747558

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703.5	97.8	206	20	AAW86202 Human VEGF-related
2	649	90.3	188	20	AAW86201 Human vascular end
3	644	89.6	188	17	AAW04826 Heart vascular end
4	644	89.6	188	20	AAW80490 Murine vascular end
5	644	89.6	206	21	AAV94806 Human VEGF-3 splice
6	644	89.6	207	17	AAW04830 Human VEGF-3 splice
7	644	89.6	207	22	AAW836296 Human vascular end
8	644	89.6	221	18	AAW07611 Human vascular end
9	644	89.6	221	18	AAV94802 Human VEGF-3. Hom
10	641	89.2	207	20	AAW80494 Murine vascular end
11	636	88.5	221	20	AAW86205 Human vascular end

12	634	88.2	188	17	AAW00864 Murine VRF167. Mu
13	634	88.2	207	17	AAW00863 Murine VRF186. Mu
14	630.5	87.7	195	17	AAW04827 Heart vascular end
15	630.5	87.7	195	20	AAW80491 Murine vascular en
16	628	87.3	189	22	AAE09217 Hexa-His-tagged hu
17	624	86.8	167	20	AAV08283 Human growth facto
18	624	86.8	167	21	AAW824082 Human PRO834 matur
19	624	86.8	186	20	AAV08282 Human growth facto
20	618	86.0	795	22	AAV029777 Novel human secret
21	616	85.7	201	17	AAW86236 Human VEGF-3 full
22	612	85.1	133	17	AAW04828 Vascular endotheli
23	612	85.1	133	20	AAW80492 Murine vascular en
24	608.5	84.6	185	20	AAW86235 Human VRF (VEGF-re
25	579	80.5	194	20	AAW86218 Human VEGF-3 trunc
26	571.5	79.5	178	20	AAW86214 Human VRF-2 trunc
27	571	79.4	167	20	AAW86234 Human VEGF-B full
28	549	76.4	160	20	AAW86208 Human VEGF-B trunc
29	548	76.2	189	20	AAW86219 Human VEGF-3 trunc
30	540.5	75.2	173	20	AAW86215 Human VRF-2 trunc
31	529	73.6	101	17	AAW00728 Vascular endotheli
32	527	73.3	155	20	AAW86209 Human VEGF-B trunc
33	520	72.3	184	20	AAW86220 Human VEGF-3 trunc
34	515	71.6	152	20	AAW86210 Human VEGF-B trunc
35	512.5	71.3	168	20	AAW86216 Human VRF-2 trunc
36	504	70.1	150	20	AAW86211 Human VEGF-B trunc
37	494	68.7	179	20	AAW86221 Human VEGF-3 trunc
38	490	68.2	147	20	AAW86212 Human VEGF-B trunc
39	489	68.0	102	17	AAW04824 Vascular endotheli
40	489	68.0	102	20	AAW80488 Murine vascular en
41	486.5	67.7	163	20	AAW86217 Human VRF-2 trunc
42	478	66.5	145	20	AAW86213 Human VEGF-B trunc
43	270.5	37.6	190	20	AAV33440 Parapox virus VEGF
44	269.5	37.5	146	13	AAW22348 Alternative form o
45	269.5	37.5	146	13	AAW27354 Sequence of vascul

ALIGNMENTS

RESULT 1	
ID	AAW86202 standard; protein; 206 AA.
XX	
AC	AAW86202:
XX	
DT	16-FEB-1999 (first entry)
XX	
DE	Human VEGF-related factor (VRF)-2 sequence.
XX	
KW	VEGF, VRF; vascular endothelial growth factor; VEGF-related protein;
KW	recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
KW	coronary; collateral vessel development; cell growth; migration; heart;
KW	lower limb ischemia; stroke; peripheral vascular disease; intestine;
KW	wound healing; skin; VEGF-related factor; VRF; vascular permeability.
XX	
OS	Homo sapiens.
XX	
PN	W09849300-A2.
XX	
PD	05-NOV-1998.
XX	
PF	20-APR-1998; 98WC-US07801.
XX	
PR	25-APR-1997; 97US-0842984.
XX	
PA	(COLL-) COLLATERAL THERAPEUTICS.
XX	
PI	Bohlen P;
XX	
DR	WPI; 1999-009426/01.
XX	
PT	New truncated vascular endothelial growth factor-related protein
PT	subunits - lack part of the N-terminal sequence, used to stimulate

PT angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Disclosure; Fig 1; 113pp; English.
XX
CC This represents the amino acid sequence of human VRP-2 (a vascular
CC endothelial growth factor (VEGF)-related factor). The invention
CC provides truncated VRP (VEGF-related protein) subunits that have at
CC least one amino acid N-terminal to the first Cys of the core sequence
CC deleted. Host cells transfected or transfected with expression vectors
CC containing nucleic acids encoding the truncated VRP subunits are used to
CC produce the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have in vivo and in vitro,
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability.
XX
SQ Sequence 206 AA;

Query Match 97.8%; Score 703.5; DB 20; Length 206;
Best Local Similarity 99.3%; Pred. No. 4,7e-66;
Matches 135; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSPLLRRLTLAALLQAPAVSOPDAPGHQKRVSWIDVYTRATCOPREVVVPLTVEL 60
DB 1 mspllrrlllvaallqlartqapvsgfdgprshqkvvswldvylratcqprrvvvpltlvel 60
QY 61 MGTVAQLVPSCVTVQRCGCCPDGDLCEVPTGQVQIIMIRYSSQLGEMSLSEHS 120
DB 61 mgtvavqlvpscvtvqrcgccpddgdlcevpptgqhvrmqimlirypssqlgemslsehs 120
QY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkdsavkpd 136
QY 121 qcecrpkkkdsavkpd 135
DB 121 qcecrpkkkdsavkpd 135

RESULT 2
AAW86201
ID AAW86201 standard; protein; 188 AA.
XX
AC AAW86201;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human vascular endothelial growth factor (VEGF)-B sequence.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN W09849300-A2.
XX
PD 05-NOV-1998.
XX
PF 20-APR-1998; 98WO-US07801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1999-009426/01.
XX
PT New truncated vascular endothelial growth factor-related protein

PT subunits - lack part of the N-terminal sequence, used to stimulate
XX angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Disclosure; Fig 1; 113pp; English.
XX
CC This represents the amino acid sequence of human vascular endothelial
CC growth factor (VEGF)-B protein. The invention provides truncated VRP
CC (VEGF-related protein) subunits that have at least one amino acid
CC N-terminal to the first Cys of the core sequence deleted. Host cells
CC transfected or transfected with expression vectors containing nucleic
CC acids encoding the truncated VRP subunits are used to produce the
CC truncated proteins recombinantly. The truncated VRP subunits, optionally
CC expressed from gene therapy vectors, have in vivo and in vitro angiogenic
CC activity and are used to stimulate angiogenesis, particularly coronary
CC collateral vessel development in cases of cardiac ischaemia; to stimulate
CC endothelial cell growth and migration in vitro; to treat heart disease;
CC to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb
CC ischaemia; stroke and peripheral vascular disease); to promote healing of
CC wounds (of skin or intestines), and to increase vascular permeability.
XX
SQ Sequence 188 AA;

Query Match 90.3%; Score 649; DB 20; Length 188;
Best Local Similarity 89.7%; Pred. No. 2.3e-60;
Matches 122; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSPLLRRLTLAALLQAPAVSOPDAPGHQKRVSWIDVYTRATCOPREVVVPLTVEL 60
DB 1 mspllrrlllvaallqlartqapvsgfdgprshqkvvswldvylratcqprrvvvpltlvel 60
QY 61 MGTVAQLVPSCVTVQRCGCCPDGDLCEVPTGQVQIIMIRYSSQLGEMSLSEHS 120
DB 61 mgtvavqlvpscvtvqrcgccpddgdlcevpptgqhvrmqimlirypssqlgemslsehs 120
QY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkdsavkpd 136
QY 121 qcecrpkkkdsavkpd 136
DB 121 qcecrpkkkdsavkpd 136

RESULT 3
AAW04826
ID AAW04826 standard; protein; 188 AA.
XX
AC AAW04826;
XX
DT 28-APR-1997 (first entry)
XX
DE Heart vascular endothelial growth factor-B167.
XX
KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
XX
OS Mus musculus.
XX
PN W09626736-A1.
XX
PD 06-SEP-1996.
XX
PF 01-MAR-1996; 96WO-US02957.
XX
PR 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX

DR WPI: 1996-412582/41.
DR N-PSDB: AAT37910.
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
XX
PS Claim 18; Page 55-56; 107pp; English.
XX
XX AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC some effects referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences, this is especially useful in retarding VEGF expression in
CC tumour cells.
XX
SQ Sequence 188 AA:

Query Match 89.6%; Score 644; DB 17; Length 188;
Best Local Similarity 89.0%; Pred. No. 7.6e-60;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSPFLRLLLAALQLAPAPVSPDAPGHQKRVSMIDVYTRACQPREVVPLTVEL 60
DB 1 mspflrrlllvalqlartqapvsgfdgshqkvvwpldyaracqprevvplsmel 60
QY 61 MGTVAKQVPSCTVQVRCGCCPDGIECVPTGQHOVROMQILMIRPSSQLGEMSLSEHS 120
DB 61 mgnvvvqqlvpsectvqvcgpcpddgilecvptgqhvymqilmlypsqigemslehs 120
QY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkkesavkpd 136

RESULT 4
AAW80490
ID AAW80490 standard; Protein: 188 AA.

XX
XX AAW80490;
XX
DT 29-JAN-1999 (first entry)
XX
DE Murine vascular endothelial growth factor (VEGF)-B167.
XX
XX Vascular endothelial growth factor; VEGF: proliferation; mouse;
XX
XX endothelial cell; angiogenesis; tissue growth; organ repair.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 1 /note="encoded by G"
XX
XX US5840693-A.
XX
XX 24-NOV-1998.
XX
PD

XX
XX 01-MAR-1996; 96US-0609443.
XX
XX 01-MAR-1996; 96US-0609443.
XX
XX 01-MAR-1995; 95US-0397651.
XX
XX 06-JUN-1995; 95US-0469427.
XX
XX 06-DEC-1995; 95US-0569063.
XX
XX (LUDM-) LUDMIG INST CANCER RES.
XX
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alltalo K, Eriksson U, Olofsson B, Pajusola K;
XX
XX WPI: 1999-034079/03.
XX
XX N-PSDB: AAV63564.
XX
XX
XX Vascular endothelial growth factor-B isoforms, and DNA encoding
XX them - useful for inducing angiogenesis and cellular proliferation,
XX and raising antibodies to inhibit activities in e.g. tumours
XX
XX Claim 1; Fig 4; 52pp; English.
XX
XX
XX The present sequence represents murine vascular endothelial growth factor
XX (VEGF)-B167. VEGF proteins are used for promoting proliferation of
XX endothelial cells and for stimulating angiogenesis (the proliferation
XX of new capillaries form pre-existing blood vessels). These activities
XX are useful for treating tissue growth and repair, including organ
XX repair. This is also useful in pregnancy, in follicle development,
XX as these processes must occur in development of the placenta. The
XX proteins can also be used to raise antibodies, either for use in
XX detection of the proteins or as inhibitors of their action. This is
XX especially useful as angiogenesis is required by tumours as they need
XX new blood supplies to grow and proliferate.
XX
SQ Sequence 188 AA:

Query Match 89.6%; Score 644; DB 20; Length 188;
Best Local Similarity 89.0%; Pred. No. 7.6e-60;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSPFLRLLLAALQLAPAPVSPDAPGHQKRVSMIDVYTRACQPREVVPLTVEL 60
DB 1 mspflrrlllvalqlartqapvsgfdgshqkvvwpldyaracqprevvplsmel 60
QY 61 MGTVAKQVPSCTVQVRCGCCPDGIECVPTGQHOVROMQILMIRPSSQLGEMSLSEHS 120
DB 61 mgnvvvqqlvpsectvqvcgpcpddgilecvptgqhvymqilmlypsqigemslehs 120
QY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkkesavkpd 136

RESULT 5
AA94806
ID AA94806 standard; Protein: 206 AA.

XX
XX AA94806;
XX
DT 19-JUN-2000 (first entry)
XX
XX Human VEGF-3 splice variant.
XX
XX Vascular endothelial growth factor 3; VEGF-3; splice variant;
XX
XX vascular expression; lymphatic; bone marrow; colon; heart; kidney; ovary;
XX
XX cancer; wounds; autoimmune disease; HIV; inflammation; heart disease.
XX
XX Homo sapiens.
XX
XX WO200009148-A1.
XX
XX 24-FEB-2000.
XX
PD

XX 10-AUG-1999; 99WO-US18054.
PF 10-AUG-1998; 98US-0132088.
PR 10-FEB-1999; 99US-0244694.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Hu J, Olsen HS, Rosen CA;
XX WPI: 2000-224173/19.
DR
XX New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
PT disorders associated with vascular and lymphatic system -
XX
XX Claim 25; Fig 4; 209pp; English.
XX
XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806), and
CC nucleic acids encoding them (AA15748, AA15762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. The present sequence represents a splice
CC variant of human VEGF-3.
XX
SQ Sequence 206 AA;
Query Match 89.6%; Score 644; DB 21; Length 206;
Best Local Similarity 100.0%; Pred. No. 8.4e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 PAQAPVSPDAPGHRKVMIDVYTRATCOPREVVVPLTVELMGTAQOLVPSCTVQR 77
Db 17 papepvsdpdpghqkrkxvswldytralcqprevvvplvelmgtaqolvpsevtqr 76
QY 78 CGGCCPDGDLCEVPTGQHQVQMILMIRYSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 77 cggccpddgdlcevpptgqhqvrmqllmitypsqjgmsleehsgcecrpkkdsavkpd 135
RESULT 6
AAW04830
ID AAW04830 standard; Protein; 207 AA.
XX
XX AAW04830;
XX
XX 28-APR-1997 (first entry)
XX
XX Vascular endothelial growth factor-B186.
XX
XX Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
XX VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
XX vascular permeability factor; cell mitogen; angiogenesis; cell growth;
XX embryonic development; wound healing; tissue reorganisation; antibody;
XX cancer; metastatic risk; tumour cell; mouse.
XX Mus musculus.
XX
XX W09626736-A1.
XX

PD 06-SEP-1996.
XX
XX 01-MAR-1996; 96WO-US02957.
XX
XX 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
XX (LUDWIG) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alltalo K, Eriksson U, Olofsson B, Pajusola K;
PI WPI: 1996-412582/41.
DR N-PSDB; AAT37914.
XX
XX Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
XX Claim 18; Page 60-61; 107pp; English.
XX
XX AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences; this is especially useful in retarding VEGF expression in
CC tumour cells.
XX
SQ Sequence 207 AA;
Query Match 89.6%; Score 644; DB 17; Length 207;
Best Local Similarity 89.0%; Pred. No. 8.5e-60;
Matches 121; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 1 MSPILRLLLAALQADPAQAPVSPDAPGHRKVMIDVYTRATCOPREVVVPLVEL 60
Db 1 mspilrllllvallyqartcpvsgfdgshqkxvswldytralcqprevvvplsmel 60
QY 61 MGTAAQOLVPSCTVQRGCGCCPDGDLCEVPTGQHQVQMILMIRYSSQLGEMSLSEHS 120
Db 61 mgnvavkqlvpsevtqrqgscpddgdlcevpptgqhqvrmqllmitypsqjgmsleehs 120
QY 121 QCECRPKKDSAVKPD 136
Db 121 qcecrpkkdsavkpd 136
RESULT 7
AAB36296
ID AAB36296 standard; Protein; 207 AA.
XX
XX AAB36296;
XX
XX 23-FEB-2001 (first entry)
XX
XX Human vascular endothelial growth factor VEGF-B186.
XX

XX Human; vascular endothelial growth factor; VEGF-B; bone growth;
KW angiogenesis; neovascularisation; bone break; inflammation.
XX
OS Homo sapiens.
XX WO20064261-A1.
PN
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-US11096.
XX
PR 26-APR-1999; 99US-0130935.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI Aase K, Kalpainen A, Olofsson B, Alltalo K, Eriksson U;
XX
DR WPI: 2001-015797/02.
XX N-PSDB; AAC81776.
XX
PT Use of a polypeptide having the biological activity of vascular
XX endothelial growth factor-B for stimulating angiogenesis of bone,
PT healing of bone fractures and enhancing acceptance of an implant to
PT bone -
XX
PS Claim 1: Page 37-38; 43pp; English.
XX
CC The present invention discloses a use for human vascular endothelial
XX growth factor B (VEGF-B) in the stimulation of angiogenesis in bone. This
CC can be used to promote bone growth, stimulate the healing of breaks or
CC fractures, secure an implant to the bone and to alleviate inflammation in
CC long bones.
XX
S0 Sequence 207 AA:

Query Match	Similarity	89.6%	Score 644	DB 22	Length 207
Best Local	Similarity	89.0%	Pred. No. 8.5e-60		
Matches 121	Conservative	5	Mismatches 10	Indels 0	Gaps 0
QY	1 MSPLRLRLAALLQAPAAQAPVSPDAPGHRKRVYSDWIDVYRATCGPREVVVPLTVEL 60				
Db	1 mspILrlllIvallqIartqapvsqfdgshqkvvpmwIdyIaracqprevvplsmel 60				
QY	61 MGTVAKQLYPSCVYVQRCGCCCPDDBLECVPTGQHOVRRMOILMIRIPSSQLGEMSLDEHS 120				
Db	61 mgnvvkqIvpscvtyrcgscpddgIecvptqhvrmqImIdgypsqIdgmsleehs 120				
QY	121 QCECRPKKKDSAVKPD 136				
Db	121 qcecrpkkkesavkpD 136				
RESULT 8					
AAW07611					
ID	AAW07611 standard; Protein; 221 AA.				
XX					
AC	AAW07611;				
XX					
DT	01-SEP-1997 (first entry)				
XX					
DE	Human vascular endothelial growth factor 3.				
XX					
KW	Human vascular endothelial growth factor; hVEGF3; angiogenesis;				
KW	tumour; inflammation; rheumatoid arthritis; diabetic retinopathy;				
KW	psoriasis; bone; periodontium; ligament; antagonist.				
XX					
OS	Homo sapiens.				
XX					
Key	Location/Qualifiers				
FH	Region				
FT	69..82				

FT	/label= PDGF/VEGF_family_signature
FT	/note= "conserved PXCvxxRxxGCCN motif"
XX	
XX	
PN	MO9639421-A1.
XX	
PD	12-DEC-1996.
XX	
PF	06-JUN-1995; 95WO-US07283.
XX	
PR	06-JUN-1995; 95WO-US07283.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
XX	
PI	Olson H, Rosen CA, Hu JS;
XX	
DR	WPI: 1997-043056/04.
DR	N-PSDB; AAT44071.
XX	
PT	DNA encoding human vascular endothelial growth factor 3 - useful to
PT	develop prods. for, e.g. stimulating angiogenesis or treating
PT	tumours, inflammation or rheumatoid arthritis
XX	
PS	Claim 11; Page 44; 56pp; English.
XX	
CC	This sequence is that of human vascular endothelial growth factor 3
CC	(VEGF3). The growth factor can be used to stimulate angiogenesis and
CC	wound healing, and to promote vascular tissue repair. It can also be
CC	used to induce the growth of damaged bone, periodontium or ligament
CC	tissue. VEGF3 antagonists can be used to inhibit tumour growth, or to
CC	treat diabetic retinopathy, inflammation, rheumatoid arthritis or
CC	psoriasis. VEGF3 is structurally related to the PDGF/VEGF family
CC	and it includes the conserved signature motif for the family (see
CC	features table).
XX	
SQ	Sequence 221 AA;

	Best Local Similarity	100.0%	Pred. No. 9.2e-60;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 119; <td>Conservative</td> <td>0;</td> <td>Mismatches 0;</td> <td>Indels 0;</td> <td>Gaps 0;</td> <td></td>	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	18	PAOAPVSDPAPGHOAKRVVSMIDVYTRATCQPREVVVPLTVELMGTVAKOLVPSCTVQR	77			
Ddb	17	pdgapvsgpdapghqrfkvswsidvylratcqprevvpltlvelmgftvakqlypscvtvqr	76			
QY	78	CGGCCPDGDLCEVPFGQHQVQKQILMIRYPSQGLEMSLEHNSQCECPKPKKDSAVKPD	136			
Ddb	77	cggccpddgdlcvpcqghqvrmqimlirypsqigemslsehsqcecrpkkkdsavkpd	135			
RESULT	9					
AAV94802	ID	AAV94802 standard; Protein; 221 AA.				
XX	XX	AAV94802;				
XX	AC					
XX	DT	19-JUN-2000 (first entry)				
XX	DE					
XX	XX	Human VEGF-3.				
KW	XX	Vascular endothelial growth factor 3; VEGF-3; vascular expression;				
KM	XX	lymphatic; bone marrow; colon; heart; kidney; ovary; cancer; wounds;				
KW	XX	autoimmune disease; HIV; inflammation; heart disease.				
OS	XX	Homo sapiens.				
PN	XX	WO200009148-A1.				
XX	PD					
XX	XX	24-FEB-2000.				
PF	XX	10-AUG-1999;	99WO-US18054.			
XX	XX					
PR	XX	10-AUG-1998;	98US-0132088.			

```

PR 10-FEB-1999; 99US-0244694.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Hu J, Olsen HS, Rosen CA;
PI
XX WPI; 2000-224173/19.
XX
XX New human gene encoding vascular endothelial growth factor 3 and
PT polypeptide encoded by the gene is useful for treating various
XX disorders associated with vascular and lymphatic system
XX
XX Claim 11: Fig 1; 209pp; English.
XX
XX The invention relates to human vascular endothelial growth factor 3
CC (VEGF-3, AAY94802), a splice variant of human VEGF-3 (AAY94806), and
CC nucleic acids encoding them (AA15748, AA15762). The cDNA encoding
CC VEGF-3 was initially isolated from a bone marrow cell line cDNA library.
CC The cDNA encoding the variant VEGF-3 differs from sequence AA15748 in
CC that the A at position 498 in AA15748 is not present in AA15762. VEGF-3
CC is also expressed in colon, heart, kidney and ovary tissues, this pattern
CC being consistent with vascular and lymphatic specific expression. VEGF-3
CC proteins and nucleotides are useful in preventing, treating or
CC ameliorating various disorders and conditions associated with the
CC vascular and lymphatic systems. These conditions and disorders include
CC cancer, wounds, autoimmune diseases, HIV, inflammation and heart
CC disease. VEGF-3 may also be used to identify its own binding partners.
CC VEGF-3 nucleotides are useful as diagnostic or prognostic markers and as
CC an alternative to restriction fragment length polymorphism (RFLP). The
CC nucleotides are also useful to prepare PCR primers for amplifying an
CC isolating selected DNAs. The present sequence represents human VEGF-3.
XX
XX Sequence 221 AA:
SQ

```

Query Match 89.6%; Score 644; DB 21; Length 221;
 Best Local Similarity 100.0%; Pred. No. 9.2e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 18 PAQAPVSOPDAPGQKRVSMIDVYTRATCQPREVVVPLTVELMGIVAKOLVPSCTVYOR 77
DB 17 padapvsqpdapghqkvsvldvytracqprevvvplvtelmgivakqlvpsctvtrq 76
OY 78 CGGCCPDGDLGECVPTGQHOVROQILMIRPSSQLGEMSLSEHSQCCRPKKDSAVKPD 136
DB 77 cgcccpdgdglecvtgqhvymqlmtrypsqlgmsleehsqccrcpkkdsavkpd 135

```

RESULT 10
 AAW80494
 ID AAW80494 standard; protein; 207 AA.
 AC AAW80494;
 XX
 DT 29-JAN-1999 (first entry)
 XX
 DE Murine vascular endothelial growth factor (VEGF)-B186.
 XX
 KW Vascular endothelial growth factor; VEGF; proliferation; mouse;
 KM endothelial cell; angiogenesis; tissue growth; organ repair.
 XX
 OS Mus sp.
 XX
 PN US5840693-A.
 PD 24-NOV-1998.
 XX
 PF 01-MAR-1996; 96US-0609443.
 XX
 PR 01-MAR-1996; 96US-0609443.
 PR 01-MAR-1996; 95US-0397651.
 PR 06-JUN-1995; 95US-0469427.
 PR 06-DEC-1995; 95US-0569063.

```

XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
XX Alitalo K, Eriksson U, Olofsson B, Pajusola K;
PI
XX WPI; 1999-034079/03.
XX
XX N-PSDB; AAV63568.
XX
XX Vascular endothelial growth factor-B isoforms, and DNA encoding
PT them - useful for inducing angiogenesis and cellular proliferation,
XX and raising antibodies to inhibit activities in e.g. tumours
XX
XX Claim 1; Fig 13; 52pp; English.
XX
XX The present sequence represents murine vascular endothelial growth factor
CC (VEGF)-B186. VEGF proteins are used for promoting proliferation of
CC endothelial cells and for stimulating angiogenesis (the proliferation
CC of new capillaries form pre-existing blood vessels). These activities
CC are useful for treating tissue growth and repair, including organ
CC repair. This is also useful in pregnancy, in follicle development,
CC as these processes must occur in development of the placenta. The
CC proteins can also be used to raise antibodies, either for use in
CC detection of the proteins or as inhibitors of their action. This is
CC especially useful as angiogenesis is required by tumours as they need
XX new blood supplies to grow and proliferate.
XX
XX Sequence 207 AA:
SQ

```

Query Match 89.2%; Score 641; DB 20; Length 207;
 Best Local Similarity 88.2%; Pred. No. 1.8e-59;
 Matches 120; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

```

OY 1 MSPLRLRLIALMLQAPAPVSOPDAPGQKRVSMIDVYTRATCQPREVVVPLTVEL 60
DB 1 msplrlrrlllvalldqatqdpavqdgshqkvwpldvyaratcqprrvvvplsmel 60
OY 61 MGVAKOLVPSCTVYORCGGCCPDGDLGECVPTGQHOVROQILMIRPSSQLGEMSLSEHS 120
DB 61 mgnvkvqilvpsctvtrcgcgccpdgdglecvtgqhvymqlmtrypsqlgmsleehs 120
OY 121 QCECRPKKKDSAVKPD 136
DB 121 qcecrpkkkesavkpd 136

```

RESULT 11
 AAW86205
 ID AAW86205 standard; protein; 221 AA.
 AC AAW86205;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human vascular endothelial growth factor (VEGF)-3 sequence.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.

XX
PI Grimmond S, Hayward NK, Larsson C, Nordenskjoeld M;
PI Weber G;
XX
DR WPI; 1996-412774/41.
XX N-PSDB; AAT13809.
XX
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
XX
PS Example 5; Fig 9; 113pp; English.
XX
CC VRF186 (AAW00863) is the murine homologue of human vascular endothelial
CC growth factor-like polypeptide SOM175 (AAW00725), a protein capable of
CC inducing astroglial proliferation and of promoting neural survival
CC and/or proliferation. Its amino acid sequence was deduced from a
CC cDNA clone (AAT13809) isolated from a new-born mouse brain cDNA
CC library. An alternatively spliced variant, VRF169 (AAW00864), was
CC also identified.
XX
SQ Sequence 207 AA:

Query Match 88.2%; Score 634; DB 17; Length 207;
Best Local Similarity 87.5%; Pred. No. 9.5e-59;
Matches 119; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSPFLRLRLIAALLOAPAPVYSDPAPGHOKRVSMIDVYRANCPREVVPPLVEL 60
Db 1 mspflrrlllvalqlartqavpsqldgphqkvwvpldyaratcprevvvpplsmel 60

QY 61 MGTVAKQLVPSCTVYORCGCCPDGILECVPTGQHGYRMOILMIRYPSQLGEMSLSEHS 120
Db 61 mgnvvkqlvpsctvgrcgccpddgilecvptghqyrmqlmlypsqlgemslgehs 120

QY 121 QCECRPKKDSAVKPD 136
Db 121 qcecrpkkkesavrp 136

RESULT 14
AAW04827
ID AAW04827 standard; Protein; 195 AA.
AC AAW04827;
XX
XX 28-APR-1997 (first entry)
XX
DE Heart vascular endothelial growth factor-B174.
XX
XX Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
XX VEGF; endothelial; mesodermal cell; cationic dimer; tissue regeneration;
XX vascular permeability factor; cell mitogen; angiogenesis; cell growth;
XX embryonic development; wound healing; tissue reorganisation; antibody;
XX cancer; metastatic risk; tumour cell; mouse.
XX
OS Mus musculus.
XX
XX W09626736-A1.
XX
XX 06-SEP-1996.
XX
XX 01-MAR-1996; 96WO-US02957.
XX
XX 06-DEC-1995; 95US-0569063.
XX 01-MAR-1995; 95US-0397651.
XX 06-JUN-1995; 95US-0469427.
XX
XX (LUDWIG-) LUDWIG INST CANCER RES.
XX (UYHE-) UNITV HELSTINKI LICENSING LTD OY.
XX
XX Aitalo K, Eriksson U, Olofsson B, Pajusola K;

XX
DR WPI; 1996-412582/41.
XX N-PSDB; AAT37911.
XX
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
PS Claim 18; Page 56-57; 107pp; English.
XX
XX AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
XX proteins of the invention, which promote endothelial or mesodermal cell
XX proliferation. VEGF is also a glycosylated cationic dimer, and is
XX sometimes referred to as vascular permeability factor (VPF). VEGF has
XX diverse effects, depending on the specific biological context in which
XX it is found. VEGF is a potent endothelial cell mitogen, and directly
XX contributes to induction of angiogenesis in vivo by promoting
XX endothelial cell growth during normal embryonic development, wound
XX healing, and tissue regeneration/reorganisation. The VEGF proteins of
XX the invention share the angiogenic and other properties of VEGF, but are
XX distributed and expressed in tissues differently to VEGF. The proteins
XX can therefore be used to accelerate angiogenesis in wound healing.
XX Antibodies against the proteins can be used for inhibiting angiogenesis.
XX The antibodies can also be used diagnostically to quantitatively detect
XX VEGF-B. Primers complementary to the coding sequences for the proteins
XX of the invention can also be used to detect VEGF-B coding sequences.
XX Quantification of VEGF-B in cancer biopsy specimens may be useful as an
XX indicator of metastatic risk. VEGF-B expression in a cell can be
XX retarded using antisense sequences direct against the VEGF coding
XX sequences, this is especially useful in retarding VEGF expression in
XX tumour cells.
SQ Sequence 195 AA:

Query Match 87.7%; Score 630.5; DB 17; Length 195;
Best Local Similarity 84.6%; Pred. No. 2.1e-58;
Matches 121; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 MSPFLRLRLIAALLOAPAPVYSDPAPGHOKRVSMIDVYRANCPREVVPPLVEL 60
Db 1 mspflrrlllvalqlartqavpsqldgphqkvwvpldyaratcprevvvpplsmel 60

QY 61 MGTVAKQLVPSCTVYORCGCCPDGILECVPTGQHGYRMOILMIRYPSQLGEMSLSEHS 113
Db 61 mgnvvkqlvpsctvgrcgccpddgilecvptghqyrmqlmlypsqlgemslgehs 120

QY 114 MSLEHSHQCECRPKKDSAVKPD 136
Db 121 mslehsqcecrpkkkesavrp 143

RESULT 15
AAW80491
ID AAW80491 standard; Protein; 195 AA.
AC AAW80491;
XX
XX 29-JAN-1999 (first entry)
XX
XX Murine vascular endothelial growth factor (VEGF)-B174.
XX
XX Vascular endothelial growth factor; VEGF; proliferation; mouse;
XX endothelial cell; angiogenesis; tissue growth; organ repair.
XX
XX Mus sp.
XX
XX US5840693-A.
XX
XX 24-NOV-1998.
XX
XX 01-MAR-1996; 96US-0609443.
XX

PR 01-MAR-1996: 96US-0609443.
PR 01-MAR-1995: 95US-0397651.
PR 06-JUN-1995: 95US-0469427.
PR 06-DEC-1995: 95US-0569063.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
XX
DR WPI: 1999-034079/03.
DR N-PSDB: AAV63565.
XX
PT Vascular endothelial growth factor-B isoforms, and DNA encoding
PT them - useful for inducing angiogenesis and cellular proliferation,
PT and raising antibodies to inhibit activities in e.g. tumours
XX
PS Claim 1: Fig 6; 52pp; English.
XX
CC The present sequence represents murine vascular endothelial growth factor
CC (VEGF)-B174. VEGF proteins are used for promoting proliferation of
CC endothelial cells and for stimulating angiogenesis (the proliferation
CC of new capillaries form pre-existing blood vessels). These activities
CC are useful for treating tissue growth and repair, including organ
CC repair. This is also useful in pregnancy, in follicle development,
CC as these processes must occur in development of the placenta. The
CC proteins can also be used to raise antibodies, either for use in
CC detection of the proteins or as inhibitors of their action. This is
CC especially useful as angiogenesis is required by tumours as they need
CC new blood supplies to grow and proliferate.
XX
SQ Sequence 195 AA;

Query Match 87.7%; Score 630.5; DB 20; Length 195;
Best Local Similarity 84.6%; Pred. No. 2.1e-58;
Matches 121; Conservative 5; Mismatches 10; Indels 7; Gaps 1;
XX
QY 1 MSPLIRLLMALIQLAQAQAVSGPDAPGHQRKRVSMIDVYTRATCQPREVYVPLTYEL 60
Db 1 msplirlllvalqlartqavsgfdgspgkqvkwvwdyvaratcprevvpltsmel 60
QY 61 MGTVAKOLVPCVTVQRCGCCPDGELCVPFGQHQRN-----QIMIRYPSQGLGE 113
Db 61 mgnvkvqglvpcvctvqrgcgcpddgilecvptgqghvrmqvgpmgqllmtypsqglge 120
QY 114 MSLEBHSQCECRPKKKDSAVKPD 136
Db 121 mslehsqcecrpkkkdsavkpd 143

RESULT 16
AAE09217
ID AAE09217 standard; Protein; 189 AA.
XX
AC AAE09217;
XX
DT 19-NOV-2001 (first entry)
XX
DE Hexa-His-tagged human VEGF-B167 protein.
XX
KW Protein purification: affinity chromatography; angiogenesis;
KW vascular endothelial growth factor; autotransplantation; tumour;
KW rheumatoid arthritis; diabetic retinopathy; His tag; human; VEGF-B167.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Region /label- leader_sequence
FT /label- Hexa-His-tag 5..10
FT Cleavage-site 14..19

FT /label= Thrombin_cleavage_site
FT Protein 22..189
FT /note= "Mature human VEGF-B167"
XX
PN WO200160861-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-A000160.
XX
PR 16-FEB-2000; 2000AU-0005681.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Scrofani SDB, Nash AD, Fabri LJ, Mackenzie AW, Scotney PD;
XX
DR WPI: 2001-541645/60.
DR N-PSDB: AAD16128.
XX
PT Purifying a protein or polypeptide, e.g. vascular endothelial growth
PT factor (VEGF)-B isoform, comprises subjecting a biological sample to
PT affinity chromatography to allow the full length to bind and not the
PT truncated or clipped forms -
XX
PS Example 1: Fig 1; 77pp; English.
XX
CC The invention relates to a method for purifying a polypeptide comprising
CC subjecting a biological sample to chromatography with an affinity matrix
CC for an N- or C-terminal region of the polypeptide, that permits binding
CC of full length molecule and not the truncated form. The method is useful
CC for purifying human vascular endothelial growth factor (VEGF) especially
CC VEGF-B isoforms e.g. VEGF-B167, VEGF-B166 and VEGF-B10-108. VEGF is
CC involved in normal angiogenesis including formation of the corpus luteum,
CC placental development, regulation of vascular permeability, inflammatory
CC angiogenesis, autotransplantation and human diseases such as tumour
CC promoting angiogenesis, rheumatoid arthritis and diabetes related
CC retinopathy. The VEGF molecules are useful in therapeutic protocols and
CC diagnostic assays. The present sequence is hexa-histidine-tagged human
CC VEGF-B167 protein.
XX
SQ Sequence 189 AA;

Query Match 87.3%; Score 628; DB 22; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.7e-58;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 21 APVSQPDAPGHQRKRVSMIDVYTRATCQPREVYVPLTYELMGTVAKOLVPCVTVQRCG 80
Db 22 apvsqpdapghqrkvsvwdytrctcprevvpltyelmgtvakqlvpcvctvqrgcg 81
QY 81 CCPDGLCECVPTGQHQRNQMILMIRYPSQGLGEMSLBHSQCECRPKKKDSAVKPD 136
Db 82 ccpdglcecvptgqhqrnmqllmtypsqglgemslbhsqcecrpkkkdsavkpd 137

RESULT 17
AAV08283
ID AAV08283 standard; Protein; 167 AA.
XX
AC AAV08283;
XX
DT 14-JUL-1999 (first entry)
XX
DE Human growth factor protein fragment VEGF-B167.
XX
KW Growth factor; human; dimer; cysteine knot; cellular inclusion body;
KW pharmaceutical.
XX
OS Homo sapiens.
XX
PN DE19748734-A1.

XX 06-MAY-1999.
 PD
 XX 05-NOV-1997; 97DE-1048734.
 PF
 XX 05-NOV-1997; 97DE-1048734.
 PR
 XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PA
 XX Erdmann H, Kaerst U, Mueller C, Rinas U, Welch H;
 PI
 XX WPI; 1999-278785/24.
 DR
 XX
 PT Preparing active growth factor dimers from inclusion bodies in high
 PT yield
 PS
 PS Claim 14; Page 8; 14pp; German.
 XX
 CC This invention describes the novel preparation of biologically active
 CC dimers of recombinant human growth factors of the cysteine knot family
 CC starting from cellular inclusion bodies. Such dimers are are useful in
 CC pharmaceutical compositions and the method provides yields of 31-39.7%,
 CC in examples, compared with about 10% for the conventional method (see
 CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
 CC protein fragments used in the method of the invention.
 CC
 XX
 SQ Sequence 186 AA;

Query Match 86.8%; Score 624; DB 20; Length 186;
 Best Local Similarity 100.0%; Pred. No. 9.5e-58;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 PVSQPDAGHQKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCVTVORCGC 81
 Db 1 pvsqpdagbhqrvswidyltracqprevvpltlvelmgvbkqlvpscvtlvgrcgsc 60
 OY 82 CPDDLECVPTGOHQRMOILMIRPSSQLGEMSLSEHSQCCECRPKKDSAYKPD 136
 Db 61 cpddlgiecvptgohqrmqilmlirpssqlgemslsehsqccecrpkkdsavkpd 115

RESULT 20
 AAU29777
 ID AAU29777 standard; Protein: 795 AA.
 AC AAU29777;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #268.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PS
 PS Claim 20; Page 193; 765pp; English.
 XX

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 CC
 XX
 SQ Sequence 795 AA;

Query Match 86.0%; Score 618; DB 22; Length 795;
 Best Local Similarity 86.7%; Pred. No. 2.3e-56;
 Matches 117; Conservative 2; Mismatches 4; Indels 12; Gaps 1;

OY 14 LQLAQAQAVSQPDAGHQKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCV 73
 Db 446 lqltqapvsqpdagbhqrvswidyltracqprevvpltlvelmgvbkqlvpscv 505
 OY 74 TVQRGCGCCPDGDLCEVPTGOHQR-----MQILMIRPSSQLGEMSLSEHSQ 121
 Db 506 tvqrgcgccpddglcevpptgohqrmqilmlirpssqlgemslsehsq 565
 OY 122 CECRPRKKDSAYKPD 136
 Db 566 cecrpkkdsavkpd 580

RESULT 21
 AAW86236
 ID AAW86236 standard; Protein: 201 AA.
 AC AAW86236;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VEGF-3 full length sequence.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 OS Homo sapiens.
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 PI Bohlen P;
 XX

DR WPI: 1999-009426/01.
XX
XX New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Claim 5; Fig 2C; 113pp; English.
XX
XX The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have in vivo and in vitro
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW86234 to AAW86239 represent full length VRP
CC sequences from which the truncated fragments are created.
XX
SQ Sequence 201 AA;

Query Match 85.7%; Score 616; DB 20; Length 201;
Best Local Similarity 99.1%; Pred. No. 7.2e-57;
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 PVSQPDAPGHRKVVSMIDYTRATCOPREVVPPLVVELMGTVAKOLVSCVTVQRCGCG 81
DB 1 pvsqpdapghrkvvsmidyttracoprevvplvvelmgtlvakqlvpscvtvqrcgcg 60

QY 82 CPDGGLECVPTGQHQVMOQLMIRYPSQSGEMLEHSGOCECPKPKKDSAVKPD 136
DB 61 cpdgglecvptgqhqvrmqlimlirypsqsqgemlsqcecrpkkkdsavkd 115

RESULT 22
AAW04828 standard; Protein: 133 AA.
XX
AC AAW04828;
XX
DT 28-APR-1997 (first entry)
XX
DE Vascular endothelial growth factor-B112.
XX
KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
XX
OS Mus musculus.
XX
XX W09626736-A1.
XX
PD 06-SEP-1996.
XX
PF 01-MAR-1996; 96MO-US02957.
XX
XX 06-DEC-1995; 95US-0569063.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
XX
PA (LUDM-) LUDMIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
XX

DR WPI: 1996-412582/41.
DR N-PSDB: AAT37912.
XX
XX Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
XX
PS Claim 18; Page 58; 107pp; English.
XX
XX AAW04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences, this is especially useful in retarding VEGF expression in
XX tumour cells.
XX
SQ Sequence 133 AA;

Query Match 85.1%; Score 612; DB 17; Length 133;
Best Local Similarity 89.1%; Pred. No. 1.2e-56;
Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSPLRLRLAALQLAPAGAPVSQDPAPGHRKVVSMIDYTRATCOPREVVPPLVVEL 60
DB 1 msplrrlllvalqlartqpsqfghshqkvrvpwidytaratcprevvplsmel 60

QY 61 MGTVALKOLVPSCVTVQRCGCGCPDGLBCVPTGQHQVMOQLMIRYPSQSGEMLEHSG 120
DB 61 mgtvavkqlvpscvtvqrcgcpdglbcvptgqhqvrmqlimlirypsqsqgemlshehs 120

QY 121 QCCECRPKKK 129
DB 121 qccecrpkkk 129

RESULT 23
AAW80492 standard; Protein: 133 AA.
XX
AC AAW80492;
XX
DT 29-JAN-1999 (first entry)
XX
DE Murine vascular endothelial growth factor (VEGF)-B112.
XX
XX Vascular endothelial growth factor; VEGF; proliferation; mouse;
KW vascular endothelial cell; angiogenesis; tissue growth; organ repair.
XX
OS Mus sp.
XX
XX US5840693-A.
XX
PN 24-NOV-1998.
XX
PD 01-MAR-1996; 96US-0609443.
PF 01-MAR-1996; 96US-0609443.
XX
PR 01-MAR-1996; 96US-0609443.
XX

PR 01-MAR-1995; 95US-0397651.
 PR 06-JUN-1995; 95US-0469427.
 PR 06-DEC-1995; 95US-0569063.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Aittalo K, Eriksson U, Olofsson B, Pajusola K;
 XX
 XX WPI: 1999-034079/03.
 DR N-PSDB: AAV63566.
 XX
 XX Vascular endothelial growth factor-B isoforms, and DNA encoding
 PT them - useful for inducing angiogenesis and cellular proliferation,
 PT and raising antibodies to inhibit activities in e.g. tumours
 XX
 PS Claim 1; Fig 8; 52pp; English.
 XX
 CC The present sequence represents murine vascular endothelial growth factor
 CC (VEGF)-B112. VEGF proteins are used for promoting proliferation of
 CC endothelial cells and for stimulating angiogenesis (the proliferation
 CC of new capillaries from pre-existing blood vessels). These activities
 CC are useful for treating tissue growth and repair, including organ
 CC repair. This is also useful in pregnancy, in follicle development,
 CC as these processes must occur in development of the placenta. The
 CC proteins can also be used to raise antibodies, either for use in
 CC detection of the proteins or as inhibitors of their action. This is
 CC especially useful as angiogenesis is required by tumours as they need
 CC new blood supplies to grow and proliferate.
 CC
 XX Sequence 133 AA;
 SQ

Query Match 85.1%; Score 612; DB 20; Length 133;
 Best Local Similarity 89.1%; Pred. No. 1.2e-56;
 Matches 115; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 OY 1 MSPLLRLLLAALLQLAAPVSGPDAPGHORKVSMDVYTRATCQPREVYVPLTVEL 60
 Db 1 MSPLLRLLVALLQIARTGVSQFQDPSHQKVPWIDYATACQPREVYVPLSMEI 60
 OY 61 MGTAKQIVPSCVTVORCGCCPDGDLCEVPTGQHVMQILMIRYSSQLGEMSLSEHS 120
 Db 61 MGNVVKQIVPSCVTVORCGCCPDGDLCEVPTGQHVMQILMIRYSSQLGEMSLSEHS 120
 OY 121 QCECRPKKK 129
 Db 121 qcecrpkkk 129

RESULT 24
 AAW86235
 ID AAW86235 standard; protein; 185 AA.
 XX
 AC AAW86235;
 XX
 XX 16-FEB-1999 (first entry)
 DE Human VRF (VEGF-related factor)-2 full length sequence.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability; VRF.
 XX
 OS Homo sapiens.
 XX
 PN W09849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX

XX
 PR 25-APR-1997; 97US-0842964.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 PA Bohlen P;
 PI
 XX
 DR WPI: 1999-009426/01.
 XX
 XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 PS Claim 5; Fig 2B; 113pp; English.
 XX
 CC The invention relates to truncated VRF (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRF subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRF subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86234 to AAW86239 represent full length VRF
 CC sequences from which the truncated fragments are created.
 CC
 XX Sequence 185 AA;
 SQ

Query Match 84.6%; Score 608.5; DB 20; Length 185;
 Best Local Similarity 99.1%; Pred. No. 4e-56;
 Matches 114; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 OY 22 PYSGPDAPGHORKVSMDVYTRATCQPREVYVPLTVELMGTAKQIVPSCVTVORCGC 81
 Db 1 PYSGPDAPGHQKVPWIDYTRATCQPREVYVPLTVELMGTAKQIVPSCVTVORCGC 60
 OY 82 CPDDGLECVPTGQHVMQILMIRYSSQLGEMSLSEHSQCRCRPPKKSAYKPD 136
 Db 61 CPDDGLECVPTGQHVMQILMIRYSSQLGEMSLSEHSQCRCRPPKKSAYKPD 114

RESULT 25
 AAW86218
 ID AAW86218 standard; protein; 194 AA.
 XX
 AC AAW86218;
 XX
 XX 16-FEB-1999 (first entry)
 DE Human VEGF-3 truncated fragment 1.
 XX
 KW VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN W09849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX

PA (COLL-) COLLATERAL THERAPEUTICS.
 XX Bohlen P;
 XX WPI; 1999-009426/01.
 DR
 XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 PS Claim 5; Fig 2C; 113pp; English.
 XX
 XX The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia, stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAM86218 to AAM86221 represent truncated
 CC fragments of VEGF-3.
 XX
 SQ Sequence 194 AA;
 XX
 Query Match 80.5%; Score 579; DB 20; Length 194;
 Best Local Similarity 99.1%; Pred. No. 5.4e-53;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 29 PGHQRKVVSMIDYTRATCPREVVPVLYEIMGTAKQLVPSCVTYQRCGCCPDGLE 88
 Db 1 pgnrkvsvwldvytracqprevvplvvelngtvakqlvpscvtvrgcgccpddgle 60
 QY 89 CVPTGOHVBMQILMIRYPSQLGEMSLERHSCCECRPKKDSAVKPD 136
 Db 61 cvptgqhvrmqilmlirypssqlgemslersqcecrpkkdsavkpd 108
 RESULT 26
 AAM86214
 ID AAM86214 standard; protein; 178 AA.
 XX
 AC AAM86214;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VRF-2 truncated fragment 1.
 XX
 XX VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; VEGF-related factor; VRP; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX Bohlen P;
 PT WPI; 1999-009426/01.

XX
 DR WPI; 1999-009426/01.
 XX
 PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX
 PS Claim 5; Fig 2B; 113pp; English.
 XX
 XX The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAM86214 to AAM86217 represent truncated
 CC fragments of VRF-2 (VEGF-related factor).
 XX
 SQ Sequence 178 AA;
 XX
 Query Match 79.5%; Score 571.5; DB 20; Length 178;
 Best Local Similarity 99.1%; Pred. No. 3e-52;
 Matches 107; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 29 PGHQRKVVSMIDYTRATCPREVVPVLYEIMGTAKQLVPSCVTYQRCGCCPDGLE 88
 Db 1 pgnrkvsvwldvytracqprevvplvvelngtvakqlvpscvtvrgcgccpddgle 60
 QY 89 CVPTGOHVBMQILMIRYPSQLGEMSLERHSCCECRPKKDSAVKPD 136
 Db 61 cvptgqhvrmqilmlirypssqlgemslersqcecrp-kkdsavkpd 107
 RESULT 27
 AAM86234
 ID AAM86234 standard; protein; 167 AA.
 XX
 AC AAM86234;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VEGF-B full length sequence.
 XX
 XX VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX Bohlen P;
 PT WPI; 1999-009426/01.
 XX

PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Claim 5; Fig 2a; 113pp; English.
XX
CC The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC optionally expressed from gene therapy vectors, have in vivo and in vitro
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW86234 to AAW86239 represent full length VRP
CC sequences from which the truncated fragments are created.
CC
SQ Sequence 167 AA;

Query Match 79.4%; Score 571; DB 20; Length 167;
Best Local Similarity 90.4%; Pred. No. 3.1e-52;
Matches 104; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 22 PVSQPDAPGHRKVVSMIDYTRATCPREVVPPLTVELMGTVAKOLPSCVTYQRCGCG 81
Db 1 pvsqfdpspsqkkyvwdytrctcqprrvvpplsmelmgvkvkqlypscvtrqrgcgc 60
QY 82 CPDDGLCVPTGQHQVMQILMIRPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 61 cpddglcvptgqhqvmqilmirpssqlgemslsehsqcecrpkkdsavkpd 115

RESULT 28
AAW86208
ID AAW86208 standard; protein; 160 AA.
XX
AC AAW86208;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human VEGF-B truncated fragment 1.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN MO9849300-A2.
XX
PD 05-NOV-1998.
XX
PF 20-APR-1998; 98WO-US07801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1999-009426/01.
XX
PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia

XX
PS Claim 5; Fig 2a; 113pp; English.
XX
CC The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC optionally expressed from gene therapy vectors, have in vivo and in vitro
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW86208 to AAW86213 represent truncated
CC fragments of VEGF-B.
CC
SQ Sequence 160 AA;

Query Match 76.4%; Score 549; DB 20; Length 160;
Best Local Similarity 91.7%; Pred. No. 6.1e-50;
Matches 99; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 29 PGHRKVVSMIDYTRATCPREVVPPLTVELMGTVAKOLPSCVTYQRCGCGCPDDGLE 88
Db 1 pshqkkyvwdytrctcqprrvvpplsmelmgvkvkqlypscvtrqrgcgcddggle 60
QY 89 CVPFGQHVQRMQILMIRPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
Db 61 cvpfgqhvqrmqilmirpssqlgemslsehsqcecrpkkdsavkpd 108

RESULT 29
AAW86219
ID AAW86219 standard; protein; 189 AA.
XX
AC AAW86219;
XX
DT 16-FEB-1999 (first entry)
XX
DE Human VEGF-3 truncated fragment 2.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN MO9849300-A2.
XX
PD 05-NOV-1998.
XX
PF 20-APR-1998; 98WO-US07801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (COLL-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1999-009426/01.
XX
PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia
PS Claim 5; Fig 2C; 113pp; English.

CC The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia), stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86218 to AAW86221 represent truncated
 CC fragments of VEGF-3.

SO Sequence 189 AA:

Query Match 76.2%; Score 548; DB 20; Length 189;
 Best Local Similarity 99.0%; Pred. No. 9.5e-50;
 Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 KVVSMIDVYTRATCOPREVVPPLTVELMGTVAKQLVPSCVTVORCGCCPDDELCEVPTG 93
 |||||||
 Db 1 kvvswldvylratcqprrvvppltlvmlgtvakqlvpscvtvgrcgccpddgilecvptg 60
 OY 94 OHQVRMOIIMIRYSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||||
 Db 61 qhvrmqllimlirypssqjgmslehsqcecrpkksavkpd 103

RESULT 30
 AAW86215
 ID AAW86215 standard; protein; 173 AA.

AC AAW86215;

DT 16-FEB-1999 (first entry)

DE Human VRF-2 truncated fragment 2.

XX VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
 KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
 KM coronary; collateral vessel development; cell growth; migration; heart;
 KM lower limb ischemia; stroke; peripheral vascular disease; intestine;
 KM wound healing; skin; VEGF-related factor; VRF; vascular permeability.

XX Homo sapiens.

PN WO9849300-A2.

PD 05-NOV-1998;

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

XX (COLL-) COLLATERAL THERAPEUTICS.

PI Bohlen P;

DR WPI; 1999-009426/01.

XX New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischemia
 PS Claim 5; Fig 2B; 113pp; English.

CC The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host

CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia), stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86214 to AAW86217 represent truncated
 CC fragments of VRF-2 (VEGF-related factor).

SO Sequence 173 AA:

Query Match 75.2%; Score 540.5; DB 20; Length 173;
 Best Local Similarity 99.0%; Pred. No. 5.3e-49;
 Matches 102; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 34 KVVSMIDVYTRATCOPREVVPPLTVELMGTVAKQLVPSCVTVORCGCCPDDELCEVPTG 93
 |||||||
 Db 1 kvvswldvylratcqprrvvppltlvmlgtvakqlvpscvtvgrcgccpddgilecvptg 60
 OY 94 OHQVRMOIIMIRYSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||||
 Db 61 qhvrmqllimlirypssqjgmslehsqcecrp-kksavkpd 102

RESULT 31
 AAW00728
 ID AAW00728 standard; protein; 101 AA.

AC AAW00728;

DT 30-NOV-1996 (first entry)

DE Vascular endothelial growth factor-like protein SOM175-e4.

XX Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;

KM astroglial proliferation.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Peptide 1..21

FT /label= Sig-peptide

PN WO9627007-A1.

PD 06-SEP-1996.

PF 22-FEB-1996; 96WO-AU00094.

PR 22-DEC-1995; 95AU-0007274.

PR 02-MAR-1995; 95AU-0001457.

PR 20-NOV-1995; 95AU-0006647.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;

PI Weber G;

DR WPI; 1996-412774/41.

DR N-PSDB; AAT33613.

XX New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival

PS Claim 14; Page 48; 113pp; English.

XX Splice variants (AAW00726-28) of the human vascular endothelial growth

CC factor-like polypeptide SOM175 (see also AAM00725) are products of
 CC cDNA clones (see also AAT33611-13) respectively lacking exon 6, exons
 CC 6-7, and exon 4 of the SOM175 gene (see also AAT33610). They show at
 CC least 1 of the properties of SOM175 including the ability to induce
 CC proliferation of vascular endothelial cells, to interact with
 CC flt-1/flk-1 receptors, and to induce cell migration, cell survival
 CC and/or an increase in intracellular levels of alkaline phosphatase.
 CC Recombinant SOM175 proteins can be used to induce astroglial
 CC proliferation and to promote neural survival and/or proliferation.
 CC
 XX Sequence 101 AA:

Query Match 73.6%; Score 529; DB 17; Length 101;
 Best Local Similarity 100.0%; Pred. No. 4,5e-48;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPLRLRLAALQLAPAPVSPDPAPGHQRVSNIDYTRATCPREVVPLVEL 60
 Db 1 msplrlrlaallqlapapvsgpdapghqrkvsidyttratcqprrvvplvel 60
 QY 61 MGTVAKQLVPSCVTVQRCGCCPDGLEGVPTGHOVARMQ 100
 Db 61 mgtvakqlvpscvtvqrcgccpddglegvptgqhgyrmq 100

RESULT 32

AAM86209
 ID AAM86209 standard; protein; 155 AA.

XX AAM86209;
 XX

DT 16-FEB-1999 (first entry)
 XX

DE Human VEGF-B truncated fragment 2.
 XX

KM VEGF: VRF: vascular endothelial growth factor; VEGF-related protein;
 KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KM coronary; collateral vessel development; cell growth; migration; heart;
 KM lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KM wound healing; skin; vascular permeability.
 XX

OS Homo sapiens.
 XX

PN W09849300-A2.
 XX

PD 05-NOV-1998.
 XX

PF 20-APR-1998; 98WO-US07801.
 XX

PR 25-APR-1997; 97US-0842984.
 XX

PA (COLL-) COLLATERAL THERAPEUTICS.
 XX

PI Bohlen P;
 XX

DR WPI; 1999-009426/01.
 XX

PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX

PS Claim 5; Fig 2a; 113pp; English.
 XX

CC The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to

CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAM86208 to AAM86213 represent truncated
 CC fragments of VEGF-B.
 CC
 XX Sequence 155 AA:

Query Match 73.3%; Score 527; DB 20; Length 155;
 Best Local Similarity 93.2%; Pred. No. 1.2e-47;
 Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 34 KVSMDYTRATCPREVVPLVELMGTVAKQLVPSCVTVQRCGCCPDGLEGVPTG 93
 Db 1 kvspmdyttratcqprrvvplsmelngmvkqlvpscvtvqrcgccpddglegvptg 60
 QY 94 OHQVMOITMIRYPSOLGEMSLFEHSQCEGRPKKDSAVKPD 136
 Db 61 qhqvrmqilimlqypsqliemslfehsqcegrpkkesavkpd 103

RESULT 33

AAM86220
 ID AAM86220 standard; protein; 184 AA.

XX AAM86220;
 XX

DT 16-FEB-1999 (first entry)
 XX

DE Human VEGF-3 truncated fragment 3.
 XX

KM VEGF: VRF: vascular endothelial growth factor; VEGF-related protein;
 KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
 KM coronary; collateral vessel development; cell growth; migration; heart;
 KM lower limb ischaemia; stroke; peripheral vascular disease; intestine;
 KM wound healing; skin; vascular permeability.
 XX

OS Homo sapiens.
 XX

PN W09849300-A2.
 XX

PD 05-NOV-1998.
 XX

PF 20-APR-1998; 98WO-US07801.
 XX

PR 25-APR-1997; 97US-0842984.
 XX

PA (COLL-) COLLATERAL THERAPEUTICS.
 XX

PI Bohlen P;
 XX

DR WPI; 1999-009426/01.
 XX

PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischaemia
 XX

PS Claim 5; Fig 2C; 113pp; English.
 XX

CC The invention relates to truncated VRP (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transformed or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRP subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRP subunits,
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischaemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischaemia; stroke and peripheral vascular disease); to promote

CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86218 to AAW86221 represent truncated
 CC fragments of VEGF-3.
 XX
 SQ Sequence 184 AA:

Query Match 72.3%; Score 520; DB 20; Length 184;
 Best Local Similarity 99.0%; Pred. No. 8.1e-47;
 Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 IDVYTRATCQPREVVVPLTVELMGTVAKOLVPSCTVYQRCGCCPDGEGCVPFGOHQVR 98
 |||||||
 Db 1 IDVYTRATCQPREVVVPLTVELMGTVAKOLVPSCTVYQRCGCCPDGEGCVPFGQHVR 60
 |||||||

QY 99 MQILMIRYPSQSGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||||
 Db 61 mqilmlirypsqsqsgemslsehsqcecrpkksavkqd 98
 |||||||

RESULT 34
 AAW86210
 ID AAW86210 standard; protein; 152 AA.
 XX
 AC AAW86210;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VEGF-B truncated fragment 3.
 XX
 KW VEGF: VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 PI Bohlen P;
 XX
 DR WPI: 1999-009426/01.
 XX
 PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischemia
 XX
 PS Claim 5; Fig 2A; 113pp; English.
 XX
 CC The invention relates to truncated VRF (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRF subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRF subunits
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86208 to AAW86213 represent truncated
 CC fragments of VEGF-B.

XX
 SQ Sequence 152 AA:

Query Match 71.6%; Score 515; DB 20; Length 152;
 Best Local Similarity 93.9%; Pred. No. 2.2e-46;
 Matches 93; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 38 MIDVYTRATCQPREVVVPLTVELMGTVAKOLVPSCTVYQRCGCCPDGEGCVPFGOHQVR 97
 |||||||
 Db 2 MIDVYTRATCQPREVVVPLTVELMGTVAKOLVPSCTVYQRCGCCPDGEGCVPFGQHVR 61
 |||||||

QY 98 MQILMIRYPSQSGEMSLSEHSQCECRPKKDSAVKPD 136
 |||||||
 Db 62 rmqilmlirypsqsqsgemslsehsqcecrpkksavkpd 100
 |||||||

RESULT 35
 AAW86216
 ID AAW86216 standard; protein; 168 AA.
 XX
 AC AAW86216;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human VRF-2 truncated fragment 3.
 XX
 KW VEGF: VRF; vascular endothelial growth factor; VEGF-related protein;
 KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
 KW coronary; collateral vessel development; cell growth; migration; heart;
 KW lower limb ischemia; stroke; peripheral vascular disease; intestine;
 KW wound healing; skin; VEGF-related factor; VRF; vascular permeability.
 XX
 OS Homo sapiens.
 XX
 PN WO9849300-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 20-APR-1998; 98WO-US07801.
 XX
 PR 25-APR-1997; 97US-0842984.
 XX
 PA (COLL-) COLLATERAL THERAPEUTICS.
 XX
 PI Bohlen P;
 XX
 DR WPI: 1999-009426/01.
 XX
 PT New truncated vascular endothelial growth factor-related protein
 PT subunits - lack part of the N-terminal sequence, used to stimulate
 PT angiogenesis, e.g. for treating heart disease and ischemia
 XX
 PS Claim 5; Fig 2B; 113pp; English.
 XX
 CC The invention relates to truncated VRF (vascular endothelial growth
 CC factor (VEGF)-related protein) subunits that have at least one amino
 CC acid N-terminal to the first Cys of the core sequence deleted. Host
 CC cells transfected or transfected with expression vectors containing
 CC nucleic acids encoding the truncated VRF subunits are used to produce
 CC the truncated proteins recombinantly. The truncated VRF subunits
 CC optionally expressed from gene therapy vectors, have in vivo and in vitro
 CC angiogenic activity and are used to stimulate angiogenesis, particularly
 CC coronary collateral vessel development in cases of cardiac ischemia; to
 CC stimulate endothelial cell growth and migration in vitro; to treat heart
 CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
 CC lower limb ischemia; stroke and peripheral vascular disease); to promote
 CC healing of wounds (of skin or intestines), and to increase vascular
 CC permeability. Sequences AAW86214 to AAW86217 represent truncated
 CC fragments of VRF-2 (VEGF-related factor).
 XX
 SQ Sequence 168 AA:

Query Match	71.3%;	Score 512.5;	DB 20;	Length 168;
Best Local Similarity	99.08;	Pred. No. 4.5e-46;		
Matches 97;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

QY IDYVTRATCPREVVVPLVLEVMGTVAAOLVPSCTVWVGCGCCPDGEGECVPTGGHOVR 98
 Db 1 IDYVTRATCGPREVVVPLVLEVMGTVAAQLVPSCVTVVVGCGCCPDGEGECVPTGGHOVR 60
 QY MQLIMLRPSSQLGEMSLSEHSQCCECRPKKDDSAVRK 136
 Db 99 MQLIMLRPSSQLGEMSLSEHSQCCECRPKKDDSAVRK 136
 QY 61 MQLIMLRPSSQLGEMSLSEHSQCCECRPKKDDSAVRK 97
 Db 61 MQLIMLRPSSQLGEMSLSEHSQCCECRPKKDDSAVRK 97

RESULT 36

ID AAW86211 standard; protein; 150 AA.

AC AAW86211;

DT 16-FEB-1999 (first entry)

DE Human VEGF-B truncated fragment 4.

KM VEGF: VEGF-vascular endothelial growth factor VEGF-related protein;
KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischemia;
KM coronary; collateral vessel development; cell growth; migration; heart
KM lower limb ischemia; stroke; peripheral vascular disease; intestine;
KM wound healing; skin; vascular permeability.

OS Homo sapiens.

PN W09849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS

PI Bohlén P.;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia

PS Claim 5; Fig 2A; 113pp; English.

The invention relates to truncated VRP (vascular endothelial growth factor (VEGF)-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits, optionally expressed from gene therapy vectors, have *in vivo* and *in vitro* angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration *in vitro*; to treat heart disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability. Sequences AAW86208 to AAW86213 represent truncated fragments of VEGF-B.

SQ Sequence 150 AA;

Query Match	Score	DB	Length
Best Local Similarity	70.1%;	504;	20;
	93.9%;	Pred. No. 3.1e-45;	

Matches	92;	Conservative	4;	Mismatches	2;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy	Db	Qy	Db
39	1	99	61
IDVYTRATCOPEVVVPLVLVETMGHVAIOAI	idvYtrAtcQpRvVvPlVsmElmgvNvqJlVpScTtVg	MQIIMTRYPSSQLGEMSLTEHSQCCECRPKKDS	mqIImTrYpSsQlGEmSlTeHsQcCeCrPkkDs
AVCPCVYVCGGCCPDGJGLCVPYTGHOHVR	gVpCvYvCGGCCPDGJGLCVPYTGHOHVR	AVKPKKDSAVKPD	avKpKkDsAvKpD
98	60	136	98

RESULT 37

ID AAW86221 standard; protein; 179 AA.

AC AAW86221;

DT 16-FEB-1999 (first entry)

DE Human VEGF-3 truncated fragment 4.

KM VEGF: VEGF: vascular endothelial growth factor; VEGF-related protein;
KM recombinant, truncated, gene therapy; angiogenesis; cardiac ischemia;
KM coronary; collateral vessel development; cell growth; migration; heart
KM lower limb ischemia; stroke; peripheral vascular disease; intestine;
KM wound healing; skin; vascular permeability.

OS Homo sapiens

PN W09849300-A2

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS.

PI Bohlén P;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate angiogenesis, e.g. for treating heart disease and ischaemia

PS Claim 5; Fig 2C; 113pp; English.

CC The invention relates to truncated VPR (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VPR subunits are used to produce
CC the truncated proteins recombinantly. The truncated VPR subunits,
CC optionally expressed from gene therapy vectors, have *in vivo* and *in vitro*
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischemia; to
CC stimulate endothelial cell growth and migration *in vitro*; to treat heart
CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischemia; stroke and peripheral vascular diseases); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW862218 to AAW86221 represent truncated
CC fragments of VEGF-3.

SQ Sequence 179 AA;

Query Match	68.7%	Score 494	DB 20	Length 179
Best Local Similarity	98.9%	Pred No. 4.3e-44		
Matches 92	Conservative 0	Mismatches 1	Indels 0	Gaps 0
44	RATCPREVVPFLVETLIMGTAVAKOLVSPCVATVORCGGCCPDDGLCEVPVGGHOVNRMOILM			103

QY 44 RATCQPREVVPLTVEIMGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHVRMQILM 103

Db 1 ratcprevvplvtelmgltvakqlypvcvtvrgcgccpddglcevpqgvtvrmqilm 60
|
OY 104 IRYPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
|
Db 61 lrypsqqlgmsllehsqccrpkksavkqd 93
|

RESULT 38

AAM86212

ID AAM86212 standard: protein; 147 AA.

XX AAM86212;

DT 16-FEB-1999 (first entry)

DE Human VEGF-B truncated fragment 5.

XX VEGF: VRF; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KW wound healing; skin; vascular permeability.

XX Homo sapiens.

XX MO9849300-A2.

XX 05-NOV-1998.

XX 20-APR-1998; 98WO-US07801.

XX 25-APR-1997; 97US-0842984.

XX (COLL-) COLLATERAL THERAPEUTICS.

XX Bohnen P;

XX WPI; 1999-009426/01.

XX New truncated vascular endothelial growth factor-related protein
PT subunits - lack part of the N-terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia

XX Claim 5; Fig 2A; 113pp; English.

XX The invention relates to truncated VRF (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transfected or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRF subunits are used to produce
CC the truncated proteins recombinantly. The truncated VRF subunits,
CC optionally expressed from gene therapy vectors, have in vivo and in vitro
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischaemia; to
CC stimulate endothelial cell growth and migration in vitro; to treat heart
CC disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAM86208 to AAM86213 represent truncated
CC fragments of VEGF-B.

XX Sequence 147 AA;

Query Match 68.2%; Score 490; DB 20; Length 147;
Best Local Similarity 93.7%; Pred. No. 8.9e-44;

Matches 89; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 42 YTRATCPREVVVPLTVELMGVTAQOLVPSCTVORCGCCDDDLCEVPGQHOVRMOI 101
|
Db 1 ytracpcrevvvplsmelmgvtaqolvpvcvtvrgcgccpddglcevpqgvtvrmqil 60
|

OY 102 IMIRYPSSQLGEMSLSEHSQCECRPKKDSAVKPD 136
|
Db 61 lmyipsqqlgmsllehsqccrpkksavkqd 95
|

RESULT 39

AAM04824

ID AAM04824 standard: peptide; 102 AA.

XX AAM04824;

DT 28-APR-1997 (first entry)

DE Vascular endothelial growth factor fragment #1.

KW Endothelial cell; proliferation; vascular endothelial growth factor; VRF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.

XX Mus musculus.

XX MO9626736-A1.

XX 06-SEP-1996.

XX 01-MAR-1996; 96WO-US02957.

XX 06-DEC-1995; 95US-0569063.

XX 01-MAR-1995; 95US-0397651.

XX 06-JUN-1995; 95US-0469427.

XX (LUDM-) LUDMIG INST CANCER RES.

XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX Alltalo K, Eriksson U, Olofsson B, Pajusola K;

XX WPI; 1996-412582/41.

XX N-PSDB; AAT37909.

XX Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis

XX Claim 18; Page 53-54; 107pp; English.

XX AAM04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which
CC it is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting
CC endothelial cell growth during normal embryonic development, wound
CC healing, and tissue regeneration/reorganisation. The VEGF proteins of
CC the invention share the angiogenic and other properties of VEGF, but are
CC distributed and expressed in tissues differently to VEGF. The proteins
CC can therefore be used to accelerate angiogenesis in wound healing.
CC Antibodies against the proteins can be used for inhibiting angiogenesis.
CC The antibodies can also be used diagnostically to quantitatively detect
CC VEGF-B. Primers complementary to the coding sequences for the proteins
CC of the invention can also be used to detect VEGF-B coding sequences.
CC Quantification of VEGF-B in cancer biopsy specimens may be useful as an
CC indicator of metastatic risk. VEGF-B expression in a cell can be
CC retarded using antisense sequences direct against the VEGF coding
CC sequences; this is especially useful in retarding VEGF expression in
CC tumour cells.

XX Sequence 102 AA;

Query Match 68.0%; Score 489; DB 17; Length 102;

Best Local Similarity 91.8%; Pred. No. 7.3e-44;
Matches 89; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
0y      33 RKVWSMIDVYTRATCQPREVVWPLTEVLMLGTVAKOLPSCVTWVRGCGGCCPDHGECVPT 92
        | || ||||| |||||||||::||| | ||||||| ||||||| |||||||
Db      2 rpvvpidvaratcqprrvvplsmelngnkvkdlvpsscvtvgcgccpdglectvpt 61
```

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07 93 GQHVRQKQILMIRPSSQLGEMSLSEHSQCCECRPKK 12
    | | | | | | | | | | | | | | | | | | | | |
Db 62 gqhqvrmqlmldqypssqlgemslsehsqccecrpkk 98

```

RESULT	40
AAW80488	
ID	AAW80488 standard; protein; 102 AA.

AC	AAW80488;	
XX		
DT	29-JAN-1999	(first entry)
XX		
DE	Murine vascular endothelial growth factor (VEGF)-B	

KM Vascular endothelial growth factor; VEGF; proliferation; mouse; endothelial cell; angiogenesis; tissue growth; organ repair.

OS	Mus sp.
XX	
PN	US5840693-A.

PD 24-NOV-1998.

PF 01-MAR-1996; 96US-0609443.

PR 01-MAR-1996; 96US-0609443.
PR 01-MAR-1995; 95US-0397651.
PR 06-JUN-1995; 95US-0469427.
PR 06-DEC-1995; 95US-0569063.

PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;

DR WPI; 1999-034079/03.
DR N-PSDB; AAV63563.

PT Vascular endothelial growth factor-B isoforms, and DNA encoding them - useful for inducing angiogenesis and cellular proliferation, and raising antibodies to inhibit activities in e.g. tumours

PS Claim 1; Fig 1; 52pp; English.

The pre-mRNA sequence represents murine vascular endothelial growth factor (VEGF)-B. The nucleic acid sequence is translated in two different reading frames. The proteins are used for promoting proliferation of endothelial cells and for stimulating angiogenesis (the proliferation of new capillaries form pre-existing blood vessels). These activities are useful for treating tissue growth and repair, including organ repair. This is also useful in pregnancy, in follicle development, as these processes must occur in development of the placenta. The proteins can also be used to raise antibodies, either for use in detection of the proteins or as inhibitors of their action. This is especially useful as angiogenesis is required by tumours as they need new blood supplies to grow and proliferate.

..... SQ Sequence 102 AA;

Query Match	68.08; Score 489; DB 20; Length 102;
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```

best local similarity  91.0%;  Freq. NO: 1.3e-44;
Matches  89;  Conservative  3;  Mismatches  5;  Indels  0;  Gaps  0;

```

QY 33 RKKVSWIDVYTRATCQPREVVPLTVELMGTVAKQLVPSCVTVQRCGGCCPDDGLECVPT 92

```
Db      | | | | | : | | | | |  
2 rpvpwidiyaratcqprrvwpismelmgvnvkqlpvscvtvgcgqccppddglecvpt 61
```

```
QY 93 GCHQVRLQIMLRYPSSQLGENSLSEHHSQCECRPKKK 125
      |||||:|||||
Db 62 gqghvrmqlimlqypssqlgmsleehsqcecrpkkk 98
```

RESULT	41
AAW86217	
ID	AAW86217 standard; protein; 163 AA

AC	AAW86217;
XX	
DT	16-FEB-1999 (first entry)

Human VRF-2 truncated fragment 4.

KM VEGF; VRF; vascular endothelial growth factor; VEGF-related protein;
KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KM coronary; collateral vessel development; cell growth; migration; heart;
KM lower limb ischaemia; stroke; peripheral vascular disease; intestine;
KM wound healing; skin; VEGF-related factor; VRF; vascular permeability.

05 Homo sapiens.

PN W09849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS.

PI Bohlén P;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate angiogenesis, e.g. for treating heart disease and ischaemia

PS Claim 5; Fig 2B; 113pp; English.

The invention relates to truncated VRP (vascular endothelial growth factor (VEGF)-related protein) subunits that have at least one amino acid N-terminal to the first Cys of the core sequence deleted. Host cells transformed or transfected with expression vectors containing nucleic acids encoding the truncated VRP subunits are used to produce the truncated proteins recombinantly. The truncated VRP subunits, optionally expressed from gene therapy vectors, have *in vivo* and *in vitro* angiogenic activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of cardiac ischaemia; to stimulate endothelial cell growth and migration *in vitro*; to treat heart disease; to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb ischaemia; stroke and peripheral vascular disease); to promote healing of wounds (of skin or intestines), and to increase vascular permeability. Sequences AAW86214 to AAW86217 represent truncated fragments of VRF-2 (VEGF-related factor).

Sequence 163 AA;

Query Match	67.7%; Score 486.5; DB 20; Length 163;
-------------	--

```

Best Local Similarity: 98.00; Area: no. 2.00 (0.00)
Matches 92; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

Qy 44 RATCPREVVPPLTVELMGTAVAKQLPVSCVTYORCGGCCPDGLEGVPTGQHOVRMQLM 103
|||||
Db 1 ratcprevvppl tvelmgtavakqlvpscvtvqrcgcccddqlecvptgqhvrmqlm 60

```
QY      104 IRYPSQLGEMSLSEHSQCCECRPKKKDSAVKPD 136
        |||||
Db       61 lrypsqlgemslsehsqcecrp-kkdsavkpd 92
```

RESULT 42

ID	AAW85213 standard; protein; 145 AA.
1	MA
2	MA
3	MA
4	MA
5	MA
6	MA
7	MA
8	MA
9	MA
10	MA
11	MA
12	MA
13	MA
14	MA
15	MA
16	MA
17	MA
18	MA
19	MA
20	MA
21	MA
22	MA
23	MA
24	MA
25	MA
26	MA
27	MA
28	MA
29	MA
30	MA
31	MA
32	MA
33	MA
34	MA
35	MA
36	MA
37	MA
38	MA
39	MA
40	MA
41	MA
42	MA
43	MA
44	MA
45	MA
46	MA
47	MA
48	MA
49	MA
50	MA
51	MA
52	MA
53	MA
54	MA
55	MA
56	MA
57	MA
58	MA
59	MA
60	MA
61	MA
62	MA
63	MA
64	MA
65	MA
66	MA
67	MA
68	MA
69	MA
70	MA
71	MA
72	MA
73	MA
74	MA
75	MA
76	MA
77	MA
78	MA
79	MA
80	MA
81	MA
82	MA
83	MA
84	MA
85	MA
86	MA
87	MA
88	MA
89	MA
90	MA
91	MA
92	MA
93	MA
94	MA
95	MA
96	MA
97	MA
98	MA
99	MA
100	MA
101	MA
102	MA
103	MA
104	MA
105	MA
106	MA
107	MA
108	MA
109	MA
110	MA
111	MA
112	MA
113	MA
114	MA
115	MA
116	MA
117	MA
118	MA
119	MA
120	MA
121	MA
122	MA
123	MA
124	MA
125	MA
126	MA
127	MA
128	MA
129	MA
130	MA
131	MA
132	MA
133	MA
134	MA
135	MA
136	MA
137	MA
138	MA
139	MA
140	MA
141	MA
142	MA
143	MA
144	MA
145	MA

AC AAW86213;

DT 16-FEB-1999 (first entry)

Human VEGF-B truncated fragment 6.

KM VEGF; Vp;vascular endothelialgrowth factor VEGF-related protein;
KM recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KM coronary; collateral vessel development; cell growth; migration; heart;
KM lower limb ischaemia; stroke; peripheral vascular disease; Intestine;
KM wound healing; skin; vascular permeability.

OS Homo sapiens.

PN W09849300-A2.

PD 05-NOV-1998.

PF 20-APR-1998; 98WO-US07801.

PR 25-APR-1997; 97US-0842984.

PA (COLL-) COLLATERAL THERAPEUTICS

PI Bohlen P;

DR WPI; 1999-009426/01.

PT New truncated vascular endothelial growth factor-related protein subunits - lack part of the N-terminal sequence, used to stimulate angiogenesis, e.g. for treating heart disease and ischaemia

PS Claim 5; Fig 2A; 113pp; English

CC The invention relates to truncated VRP (vascular endothelial growth
CC factor (VEGF)-related protein) subunits that have at least one amino
CC acid N-terminal to the first Cys of the core sequence deleted. Host
CC cells transformed or transfected with expression vectors containing
CC nucleic acids encoding the truncated VRP subunits are used to produce
CC the truncated proteins recombinantly. The truncated VRP subunits,
CC optionally expressed from gene therapy vectors, have *in vivo* and *in vitro*
CC angiogenic activity and are used to stimulate angiogenesis, particularly
CC coronary collateral vessel development in cases of cardiac ischemia. To
CC stimulate endothelial cell growth and migration *in vitro*, to treat heart
CC disease; to treat ischemia (e.g. cardiac, chronic coronary or chronic
CC lower limb ischemia; stroke and peripheral vascular disease); to promote
CC healing of wounds (of skin or intestines), and to increase vascular
CC permeability. Sequences AAW6208 to AAW6213 represent truncated
CC fragments of VEGF-B.

SQ Sequence 145 AA;

Query Match	66.5%	Score 478	DB 20	Length 145
Best Local Similarity	93.5%	Pred. No. 1.6e-42		
Matches 87	Conservative 4	Mismatches 2	Indels 0	Gaps 0

QY 44 RATCQPREVVVPLVELMGTAKQLVPSVCVTYQRCGCCPDDGECVPPTGCHQVRMLM 103
Db 1 ratcqprrvvvplsmelmgnvkqlvpscvtvyqrcgccpddglectvptqhqvrmgilm 60

```

0Y      104  IRYPSQLGEMSLSEHSQCRCRPKKDSAVKPD 136
      1:|||||
Db      61  Iqypssqlgemslsehsqcrcrpkkkesavkpd 93

```

RESULT 43

ID	Protein; AA.
AY33440	standard; 190 AA.

AC AAY33440;

DT	13-DEC-1999 (first entry)
----	---------------------------

DE Parapox virus VEGF growth factor homologue protein fragment 7.

KW DI701; vascular endothelial growth factor; PPV-VEGF; angiogenesis;
 KW endothelial cell proliferation; gene therapy; diagnostic; tissue repair;
 KW immunomodulation; dendritic cell differentiation; DNA vaccine.

OS Parapoxvirus.

PN DE19813774-A1

PD 30-SEP-1999.

PF 27-MAR-1998; 98DE-1013774.

PR 27-MAR-1998; 98DE-1013774.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Dehio C, Roettgen M, Rziha H, Buettner M;

DR WPI; 1999-552202/47.

PT Homolog of human vascular endothelial growth factor useful for stimulating endothelial cell proliferation, e.g. for stimulating angiogenesis or tissue repair or for immunomodulation

PS Disclosure; Fig 2; 16pp; German.

This invention describes a novel polypeptide that is a paratopox virus homolog of human vascular endothelial growth factor (PVY-VEGF) and stimulates endothelial cell proliferation. The products of the invention have angiogenic activity. The polypeptide can be used in pharmaceutical compositions for therapeutic or diagnostic use, e.g., for stimulating angiogenesis or tissue repair or for immunomodulation, e.g., by stimulating endothelial cell proliferation or inhibiting dendritic cell differentiation. Nucleic acids encoding the polypeptide can be used in pharmaceutical compositions for DNA vaccination or gene therapy. This sequence represents a protein fragment of a paratopox virus D1701 vascular endothelial growth factor (VEGF) homologue.

Sequence 190 AA;

Query Match	37.68;	Score 270.5;	DB 20;	Length 190;
Best Local Similarity	45.18;	Pred. No. 1.5e-20;		
Matches	55;	Conservative	22;	Mismatches 42;
			Indels	3;
			Gaps	2

[illegible]

Qy	127	KK	128
Db	132	KK	133

Qy	127	kk	128
Db	132	kk	133

RESULT 44
AAR22348
ID AAR22348 standard; protein; 146 AA

```

XX AAR22348;
AC
XX
DT 29-JUL-1992 (first entry)
DE Alternative form of VEGF mature A-subunit with 120 amino acids.
XX
XX Rat glioma cell; GS-9L; conditioned medium; heterodimer; VEGF-11;
KM homodimer; mitogenesis; vascular repair; blood vessel implant;
KM polymerase chain reaction; alternative splicing.
XX
OS Rattus.
XX
FH Key 1.26 Location/Qualifiers
FT Peptide /label= signal
FT Protein /label= VEGF_A-subunit
FT /note= "120 amino acids long"
XX
XX EP476983-A.
PN
XX
XX 25-MAR-1992.
PD
XX
XX 18-SEP-1991; 91EP-0308489.
PF
XX
XX 21-SEP-1990; 90US-0586640.
PR
XX
XX 21-SEP-1990; 90US-0586638.
PA (MERI ) MERCK & CO INC.
XX
XX Bayne ML, Conn GL, Thomas KA;
PI
XX
XX WPI; 1992-098641/13.
DR
XX
XX N-PSDB; AAQ23039.
DR
XX
XX
XX Vascular endothelial cell growth factor II - used as coating for
PT artificial blood vessels or to promote tissue repair
XX
XX
XX Example 9; Page 14 and Fig 4; 38pp; English.
PS
XX
XX Multiple cDNAs encoding alternative forms of the VEGF A-subunit
CC were amplified using PCR primers as in AAQ23049 and AAQ23050. Three
CC sets of clones were identified. Clone #12 encoded the 164 amino acid
CC secreted form of VEGF A-subunit (see AAR22347). Clone #14 has a 135 bp
CC deletion and thus encodes a 120 amino acid form and Clone #16 has a
CC 72bp insertion and encodes a 188 amino acid mature protein (AAR22351).
CC The deleted region lies between the second base of the Asn140 codon
CC and the third base of the Arg184 codon. The 120 amino acid mature
CC protein has Asn140 converted to Lys140.
XX
XX See also AAQ23038-Q23059.
XX
XX
XX Sequence 146 AA;
SQ

```

Query Match 37.5%; Score 269.5; DB 13; Length 146;
 Best Local Similarity 43.8%; Pred. NO. 1.4e-20; Indels 5; Gaps 3;
 Matches 57; Conservative 21; Mismatches 47;

```

OY 10 LAALLQLAPQAPVSPDAPGHQR--KVVSMDVYTRATCOPREVVPLTVELMGTVAKQ 67
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 lalllylhakwsgaapltegeqkavevkvfmdygryscrptletlvdifgeydeleyl 71
OY 68 LVPECVTVQRCGCCCPDGLCVPTGQHQVQMQLMIR-YSSQLGEMSLSEHSQCCECRP 126
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
DB 72 fkpscvplmrcagcndealectvpsnvvmqlmrlkphsgqlgmsflghsrcecrp 131
OY 127 KKKSAAVKPD 136
   || :
DB 132 kk--drtkpe 139

```

```

AAR27354
ID AAR27354 standard; Protein: 146 AA.
XX
AC AAR27354;
XX
XX
DT 25-FEB-1993 (first entry)
DE Sequence of vascular endothelial cell growth factor VEGF A
XX 146 amino acid residue subunit.
DE
XX
XX Vascular development; mitogen; blood vessel;
KM vascular endothelial growth factor; neovascularisation.
XX
XX
OS Rattus.
XX
XX EP506477-A.
PN
XX
XX 30-SEP-1991.
PD
XX
XX 27-MAR-1992; 92EP-0302750.
PF
XX
XX 28-MAR-1991; 91US-0676436.
PR
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Bayne ML, Thomas KA;
PI
XX
XX WPI; 1992-325745/40.
DR
XX
XX N-PSDB; AAQ28953.
DR
XX
XX
XX Vascular endothelial cell growth factor sub-units - which stimulate
PT vascular endothelial cell growth, used for inducing tissue repair
PT and growth.
XX
XX
XX Disclosure; Fig 4; 61pp; English.
PS
XX
XX The full length coding region of the A subunit or monomer of VEGF
CC is determined from three sets of overlapping cDNA clones. Degenerate
CC oligo. primers based on the amino acid sequences
CC Phe-Met-Asp-Val-Tyr-Gln from polypeptide 142 (residues 42-47) and
CC Cys-Lys-Asn-Thr-Asp from polypeptide 138 (residues 164-168) were used
CC to PCR amplify the central region of the cDNA for VEGF A chain.
CC A single band migrating at 420 bp was gel purified, digested with SalI,
CC ligated into pGEM32f(+) and sequenced. The nucleotide sequence
CC obtained (p4238) was used to design antisense and sense PCR primers
CC to amplify the 5' and 3' ends of the cDNA. These 5' and 3' clones
CC are denoted p5-15 and pW3, respectively. In addition to the cDNA
CC coding the 164 amino acid secreted form identified by protein
CC sequencing, two alternatively spliced cDNAs encoding a 146 amino acid
CC and a 214 amino acid forms are cloned and sequenced.
XX
XX
XX Sequence 146 AA;
SQ

```

Query Match 37.5%; Score 269.5; DB 13; Length 146;
 Best Local Similarity 43.8%; Pred. NO. 1.4e-20; Indels 5; Gaps 3;
 Matches 57; Conservative 21; Mismatches 47;

```

OY 10 LAALLQLAPQAPVSPDAPGHQR--KVVSMDVYTRATCOPREVVPLTVELMGTVAKQ 67
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 lalllylhakwsgaapltegeqkavevkvfmdygryscrptletlvdifgeydeleyl 71
OY 68 LVPECVTVQRCGCCCPDGLCVPTGQHQVQMQLMIR-YSSQLGEMSLSEHSQCCECRP 126
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
DB 72 fkpscvplmrcagcndealectvpsnvvmqlmrlkphsgqlgmsflghsrcecrp 131
OY 127 KKKSAAVKPD 136
   || :
DB 132 kk--drtkpe 139

```

Job time: 3708 sec

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A:Reference number: JC4679; MUID:96183052
A:Accession: JC4679
A:Molecule type: mRNA
A:Residues: 1-207 <TOM>
A:Cross-references: GB:043836; NID:g1703480; PIDN:AAC52932.1; PID:g1314334
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the family of endothelial growth factors 167 and 186.
C:Genetics:
A:Gene: vrf
A:Map position: 19
C:Keywords: growth factor
F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-207/Product: vascular endothelial growth factor related factor #status predicted <SIG>

Query Match	89.6%	Score 644	DB 2	Length 207
Best Local Similarity	89.0%	Pred. No. 2.4e-55		
Matches 121	Conservative	5	Mismatches 10	Indels 0
			Gaps	0
OY	1 MSPLLRLLTLLAALLQAPAPAVPSQPDABGHQKRVVSWIDVYTRATQPREVVPPLTVEL	60		
Db	1 NSPLLRLTLLVALLQATQAPVPSQFDGSGHQKRVVPMIDYARATQPREVVPPLSMEL	60		
OY	61 MGTVAKQLVPSCVYVQRCGGCCPDGLEGVPPGQGHVRRQIIMIRPSSQLGEMSLTEHS	120		
Db	61 MGNVVKQLVPSCVYVQRCGGCCPDGLEGVPPGQGHVRRQIIMIRPSSQLGEMSLTEHS	120		
OY	121 QCECRPKKKDSAVKPD	136		
Db	121 QCECRPKKKESAVKPD	136		

RESULT 3
S52130
vascular endothelial growth factor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text-change 05-Nov-1999
C:Accession: S52130
R:Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growth factor
A:Reference number: S52130; MUID:95143284
A:Accession: S52130
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-190 <SHA>
A:Cross-references: GB:X61380; NID:g5587559; PIDN:CAA57143.1; PID:g5587560

Query March 37.6%; Score 270.5; DB 2; Length 190;
Best Local Similarity 45.1%; Pred. No. 4.7e-19;
Matches 55; Conservative 22; Mismatches 42; Indels 3; Gaps 2;

```
OY      10 LALLQLAPQAQPPVSQPAAPHQR--KVVSMIDVYTRATCPREYYVPLTVELMGTVAKQ 67
          ||| | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db       12 LALLLYLTHAAKMSQAAPAWECDOKPHEVVEKEMDYQYRSCYPRIETLVDPFOEYDELEYI 71
OY      68 LPVSCVTWRGCGGCCPDGEGCEVPYGQHVRMOLIMIR-YSSDGLSGEMSLSEHSQCGRP 126
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       72 FKPSGVPLMRGCGCCNDGELCECVPLEEPNITWQIKRIPRHOGHIGEMSFLOHNKCGRP 131
OY      127 KK 128
          || |
Db       132 KK 133
```

RESULT 4
A35987
glioma-derived vascular endothelial cell growth factor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C/Accession: A35987
R:Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope,

Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A:Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is
A:Reference number: A35987; MUID:90207249
A:Accession: A35987
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-190 <CON>
A:Cross-references: GB:M32167; NID:g204287; PIND:AAA41211.1; PID:g204288

Query Match	37.5%	Score 269.5;	DB 2;	Length 190;
Best Local Similarity	43.8%;	Pred. No. 5.9e-19;		
Matches 57;	Conservative 21;	Mismatches 47;	Indels 5;	Gaps 3;

[illegible]

RESULT 5
B44881
vascular endothelial growth factor-1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 05-Nov-1999
C/Accession: B44881, A43351, A61029
R/Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A/Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A/Reference number: A44881; MUID: 92274860
A/Accession: B44881
A/Molecule type: mRNA
A/Residues: 1-190 <BRE>
A/Cross-references: GB: S38083; NID: g249858; PIDN: AAB22253.1; PID: g249859
A/Experimental source: embryo
A/Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
R/Claflay, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A/Title: Vascular endothelial growth factor. Regulation by cell differentiation and a
A/Reference number: A43351; MUID: 92355593

A:Residues: 1-116; 'ER','I19-190 <CLA>
A:Cross-references: GB:W95200; NID:g202350; PIDN:AAA0547.1; PID:g202351
A>Note: sequence extracted from NCBI backbone (NCBIN:I10665, NCBIF:110675)
R:Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A>Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial
A:Reference number: A61029; MUID:91197543
A:Accession: A61029
A:Molecule type: protein
A:Residues: 27-38 <ROS>
C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein;

Query Match 37.2% Score 267.5; DB Z; Length 190;
Best Local Similarity 42.3%; Pred. No. 9,2e-19;
Matches 55; Conservative 23; Mismatches 47; Indels 5; Gaps 3;

OY 10 LALLLDLPAPQVPSOPDABGHQR--KVNSMIDVTYTRATCOPREVVVPVLVELMGTVAKQ 67
 II III I : : : : : : : : : : : : : : : :
Db 12 LALLLYLHNKAWSOAAPTTEGEOKSHEVIKMMDYORKSYSCPRTITVDIDFQEPDELEYI 71

OY 68 LVPSCVAVORGGCCPRPDGLCYPTGOHOVMOLIMLR--PPSSLOIGMSLEENSHQCSCR 126
 IIIII : : : : : : : : : : : : : : : :
Db 72 FKPSCVPLMKRCAGGCCNDALCECVFTSESNTITMOILMRKPDSQHIGEMSPFLQHRCCRCP 131


```

Oy      127 KKDSAVKPD 136
      ||
      132 KK--DRTKPE 139

RESULT      6
A44881
Vascular endothelial growth factor-3 precursor - mouse
N:Contans: vascular endothelial growth factor-2; vascular permeability factor
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: A44881; A44881; A60932; S52136
R:Breier, G.; Albrecht, U.; Sterrer, S.; Risaau, W.
Development 114, 521-532, 1992
A:Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A:Reference number: A44881; MUID:92274860
A:Accession: A44881
A:Molecule type: mRNA
A:Residues: 1-214 <BRE>
A:Cross-references: GB:S37052; NID:g249856; PIDN:AA82252.1; PID:g249857
A:Experimental source: Embryo
A:Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIPI:104678)
A:Accession: C44881
A:Molecule type: mRNA
A:Residues: 1-140,209-214 <BR2>
A:Cross-references: GB:S38100; NID:g249860; PIDN:AA82254.1; PID:g249861
A:Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBIPI:107625)
R:Clausen, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.
J. Exp. Med. 172, 1535-1545, 1990
A:Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothelial
A:Reference number: A60932; MUID:91079735
A:Accession: A60932
A:Molecule type: protein
A:Residues: 27-33 <CLA>
R:Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1224, 365-370, 1994
A:Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous im
A:Reference number: S52136; MUID:95101726
A:Accession: S52136
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-46 <SUG>
C:Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
C:Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer
F:1-56/Domain: signal sequence #status predicted <SIG>
F:27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

Query Match      37.2%; Score 267.5; DB 2; Length 214;
Best Local Similarity 42.3%; Pred. No. 1e-18;
Matches 55; Conservative 23; Mismatches 47; Indels 5; Gaps 3;

Oy      10 LALLQLAPAAQAPVSPAPRHQR--KVSMDVYTRATCQPREVVVPLVTEIMGTAKQ 67
      |||||
      12 LALLYLHNHAWSQAAPTEEGEQKSHVEIKFMDYQRYCRIFLVDIFPEYDEIYI 71
      |||||
Oy      68 LVPSCVTQRCGGCCPDGECVPYGGOHVNRQJLMIR-YPSQSGEMSLDEHSGCECRP 126
      |||||
Db      72 FKPSGVPLMKRAGCCNDALCECVPTSESNITMQLIRKIPRPHOSQHIGEMSFLOHSHCECRP 131
      |||||
Oy      127 KKDSAVKPD 136
      ||
      132 KK--DRTKPE 139

RESULT      7
B40080
Vascular endothelial growth factor precursor (version 2) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C:Accession: B40080; B33787; A33255
R:Leung, D.W.; Cachianes, G.; Kiang, W.J.; Goeddel, D.V.; Ferrara, N.

```

science 246, 1306-1309, 1989

A>Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.

A:Reference number: A40080; MUID:90069608

A:Accession: B40080

A:Molecule type: mRNA

A:Residues: 1-190 <LEU>

A:Cross-references: GB:M31836; NID:g163006; PIDN:AAA30502.1; PID:g163007

R:Tischer, E., Gospodarowicz, D., Mitchell, R., Silva, M., Schilling, J., Lau, K.; Cr

Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989

A>Title: Vascular endothelial growth factor: a new member of the platelet-derived gro

A:Reference number: A33787; MUID:90121225

A:Accession: B33787

A:Molecule type: mRNA

A:Residues: 27-190 <TIS>

A:Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809

R:Ferrara, N.; Henzel, W.J.

Biochem. Biophys. Res. Commun. 161, 851-858, 1989

A>Title: Pituitary follicular cells secrete a novel heparin-binding growth factor spe

A:Reference number: A33255; MUID:89286596

A:Accession: A33255

A:Molecule type: protein

A:Residues: 27-31 <FER>

A:Keywords: alternative splicing; glycoprotein

F:1-26/Domin: signal sequence #status predicted <SIG>

F:27-190/Product: vascular endothelial growth factor #status predicted <MAT>

F:100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.1%; Score 266.5; DB 2; Length 190;
Best Local Similarity 45.1%; Pred. No. 1.2e-18;
Matches 55; Conservative 22; Mismatches 42; Indels 3; Gaps 2;

QY 10 LALLQLAPAAQAPVSPDPARGHOR--KVVSNIDVYTRATCPREVVPLTVELMGTAQK 67
| | | | | :
Db 12 LALLLYLHNAMKQDAARPAEAGGQKRHEVVKFMDYVQRFCRPIETIVDIFQEYDEIEFI 71
| | | | | :
QY 68 LVPSCTVYQRGCGCCRPDDGLCEVTPGGHQVMQILMR-YSSOLGEMSLFEHSQCRCRP 126
| | | | | :
Db 72 FKPSCVLPARMGCCNDSELCVPTEEFNITMQIMRIKPHOSHIIGEMSFLOHMKCPCRP 131
| | | | | :
QY 127 KK 128
| |
Db 132 KK 133

RESULT 8
A41551

Vascular endothelial growth factor 206 precursor - human

N:Alternate names: vascular permeability factor

N:Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VE

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1992 #sequence.revision 28-Aug-1992 #text.change 05-Nov-1999

C:Accession: A41551; C41551; RA1551; A40454; B40454; A40079; A40080; JQ1463;

R:Houck, K.A.; Ferrara, N.; Whiner, J.; Cachianes, G.; Li, B.; Leung, D.W.

Mol. Endocrinol. 5, 1806-1814, 1991

A>Title: The vascular endothelial growth factor family: identification of a fourth mo

A:Reference number: A41551; MUID:92168017

A:Accession: A41551

A:Molecule type: mRNA

A:Residues: 1-232 <HOUI>

A:Cross-references: GB:S85192; NID:g246155; PID:g246156

A:Accession: C41551

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-140, 'N', 183-232 <HOUD>

A:Accession: RA1551

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-141, 227-232 <HOUS>

R:Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;

J. Biol. Chem. 266, 11947-11954, 1991

A>Title: The human gene for vascular endothelial growth factor. Multiple protein form

A:Reference number: A40454; MUID:91268072

A:Accession: A40454
A:Molecule type: DNA
A:Residues: 1-165,183-232 <RT1>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976; GB:M63977; GB:M63978
A:Accession: BA0454
A:Molecule type: DNA
A:Residues: 1-140,'N',183-232 <RT12>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977; GB:M63978
A:Accession: C40454
A:Molecule type: DNA
A:Residues: 1-141,227-232 <RT13>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978
R:Kleck, P.J.; Hauser, S.D.; Krivy, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.T.
Science 246, 1309-1312, 1989
A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A:Reference number: A40079; MUID:90069609
A:Accession: A40079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-165,183-232 <REC>
A:Cross-references: GB:M27281; NID:9340300; PIDN:AAA36807.1; PID:9340301
R:Leung, D.W.; Cachianes, G.; Kiang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A:Reference number: A40080; MUID:90069608
A:Accession: A40080
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140,'N',183-232 <LEU>
A:Cross-references: GB:M2977; NID:9181970; PIDN:AAA35789.1; PID:9181971
R:Weinhold, K.; Matthe, D.; Welch, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A:Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial
A:Reference number: JQ1463; MUID:92231879
A:Accession: JQ1463
A:Molecule type: mRNA
A:Residues: 1-140,'N',183-232 <WEI>
A:Cross-references: EMBL:X62568; NID:937658; PIDN:CAA44447.1; PID:937659
A:Experimental source: AIDS-Kaposi's sarcoma cell
A:Accession: JQ1464
A:Molecule type: mRNA
A:Residues: 1-140,'N',227-232 <ME2>
A:Experimental source: AIDS-Kaposi's sarcoma cell
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay
J. Biol. Chem. 264, 20017-20024, 1989
A:Title: Human vascular permeability factor. Isolation from U937 cells.
A:Reference number: A34492; MUID:90062112
A:Accession: A34492
A:Molecule type: protein
A:Residues: 27-36;43-49,'R',72-76,'Q',78-81;59-71 <CON>
A:Comment: The most common of several alternatively spliced forms is VEGF 165.
C:Genetics:
A:Gene: GDB:VEGF
A:Cross-references: GDB:132244; OMIM:192240
A:Map position: 6p21-6p12
C:Function:
A:Description: promotes fluid and protein leakage from blood vessels
C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro
F:1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20
F:1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predic
F:1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status predic
F:1-26/Domains: signal sequence #status predicted <SIG>
F:101/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 36.7%; Score 264; DB 2; Length 232;
Best Local Similarity 43.9%; Pred. No. 2.4e-18;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

10 LAALLQLPAPAPVSGPAPG---HQRVYSWIDYTRATCOPREVVPPLVTELMGTAK 66
12 LALLLYLHAKWSQAPPAEAGGQNHHEVYKMDVYQSRFETLVDFQEPDELEY 71

QY 67 QLVPCVTVQRCGCCPDGECVPTGQHOVRMQLIMIR-YPSOLGEMSLSEHSQCECR 125
DB 72 IFKPCVPLMRGCGCCNDEGECVPTSESNITMQIMRIKPHOGHIGEMSFLOHKKCECR 131
QY 126 PKK 128
DB 132 PKK 134

RESULT 9
S57956
Ovine vascular endothelial growth factor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C:Accession: S57956
R:Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.N.
submitted to the EMBL Data Library, July 1995
A:Reference number: S57956
A:Accession: S57956
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <RED>
A:Cross-references: EMBL:X89506; NID:9899350; PIDN:CAA61677.1; PID:9899351

Query Match 36.6%; Score 263.5; DB 2; Length 146;
Best Local Similarity 44.3%; Pred. No. 1.8e-18;
Matches 54; Conservative 23; Mismatches 42; Indels 3; Gaps 2;

QY 10 LAALLQLPAPAPVSGPAPGHR--KVSWSIDYTRATCOPREVVPPLVTELMGTAKQ 67
DB 12 LALLLYLHAKWSQAPPAEAGGQKPEHVKRMDVYQSRFETLVDFQEPDELEY 71
QY 68 LVPSCVTQRCGCCPDGECVPTGQHOVRMQLIMIR-YPSOLGEMSLSEHSQCECRP 126
DB 72 FKPCVPLMRGCGCCNDESLCVPTEEFNITMQIMRIKPHOSOHIGEMSFLOHKKCECRP 131
QY 127 KK 128
DB 132 KK 133

RESULT 10
A33787
Vascular endothelial growth factor (version 1) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 05-Nov-1999
C:Accession: A33787
R:Titicher, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Cr
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A:Title: Vascular endothelial growth factor: a new member of the platelet-derived gro
A:Reference number: A33787; MUID:90121225
A:Accession: A33787
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <RTIS>
A:Cross-references: GB:M33750; NID:9163810; PIDN:AAA30805.1; PID:9163811
C:Keywords: alternative splicing

Query Match 35.3%; Score 253.5; DB 2; Length 120;
Best Local Similarity 46.2%; Pred. No. 1.4e-17;
Matches 49; Conservative 20; Mismatches 34; Indels 3; Gaps 2;

QY 26 PDAPGHR--KVSWSIDYTRATCOPREVVPPLVTELMGTAKQLVPSCVVQRCGCCP 83
DB 2 PMAEGGQKPEHVKRMDVYQSRFETLVDFQEPDELEYFIRKPCVPLMRGCGCN 61
QY 84 DDGECVPTGQHOVRMQLIMIR-YPSOLGEMSLSEHSQCECRPK 128
DB 62 DESLECVPTEEFNITMQIMRIKPHOSOHIGEMSFLOHKKCECRPK 107


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C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994
C:Accession: JS0735
R:Nakahara, K.; Nishimura, H., Kuro-O, M., Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazakihara, T.; Nakamura, Y. Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A>Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascular endothelial cells
A:Reference number: JN0248; MUID:q2246970
A:Accession: JS0735
A:Molecule type: mRNA
A:Residues: 1-198 <NAK>
A>Note: This protein corresponds to the endothelial type of human A chain
C:Superfamily: platelet-derived growth factor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-89/Domain: propeptide #status predicted <PRO>
F:90-198/Product: platelet-derived growth factor A1 chain #status predicted <MAT>
```

```
Query Match      17.7%; Score 127.5; DB 2; Length 198;  
Best Local Similarity 30.3%; Pred. No. 4e+05;  
Matches 34; Conservative 24; Mismatches 46; Indels 9; Gaps 5;  
  
Oy   19 AQAPVSGPDAGGHQKKVSMIDYTRATCGREVV-VPLVELMGTAKOLV-PSCVTY 75  
       :| | | | | | | | | | | | | | | | | | | | | |  
Db    71 ARHAEKPPEPVPVRKRPT-IIEALPAICKRTVIYEIPRS-QVDPTSANFLIMPCEVE 128  
               ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Oy     76 ORGCGCCDDGLGVPGTGOHVRMQLIMRY-----PSQLGEMSLSEHSOCBC 124  
         ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db     129 KRCTGCCNTSSVKCPGRVHRSRVAKEVRRPKRKLEVQRLEHLDEAC 181  
  
RESULT 20  
B28964  
platelet-derived growth factor chain A precursor splice form 2 - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999  
C:Accession: B28964; B42002; B28122  
R:Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988  
A>Title: Platelet-derived growth factor A chain: gene structure, chromosomal location  
A:Reference number: A28964; MUID:88144463  
A:Accession: B28964  
A:Molecule type: DNA  
A:Residues: 1-196 <BOU>  
A:Cross-references: GB:M1571; GB:J03638; GB:M1984; GB:M1985; GB:M1986; GB:M1987,  
R:Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.  
Genomics 13, 257-263, 1992  
A>Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF  
A:Reference number: A42002; MUID:93307656  
A:Accession: B42002  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 152-196 <BO2>  
R:Roisman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.  
Mol. Cell. Biol. 8, 571-577, 1988  
A>Title: Structural characterization of the human platelet-derived growth factor A-chain  
A:Reference number: A28122; MUID:88174698  
A:Accession: B28122  
A:Molecule type: mRNA  
A:Residues: 1-63, 'TRD', 67-196 <ROZ>  
A:Cross-references: GB:M20488  
A>Note: The authors translated the codon ACA for residue 64 as Arg, CGT for residue 6  
C:Comment: Exon 6 is spliced out of this variant splice form. For the major splice fo  
C:Gene: GDB:PDGFA  
A:Cross-references: GDB:I20266; OMIM:173430  
A:Map position: 7p22-7p22  
C:Superfamily: platelet-derived growth factor  
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
```


QY 103 MIR-----YPSOIGEMSLSEHSEC 124
 Db 137 QVRKIEIVRKRPFKKATVTLIEDHLACKC 165

RESULT 25
 PFHUG2
 platelet-derived growth factor chain B precursor [validated] - human
 N:Alternate names: PDGF B-chain; PDGF-B; PDGF-II; PDGF-related transforming protein (sis)
 C:Species: Homo sapiens (man)
 C:Date: 18-Apr-1984 #sequence, revision 20-Sep-1984 #text, change 08-Dec-2000
 R:Accession: A94276; A21024; A23532; A93366; A25141; A94271; A93308; A43499; S56115; 157
 R:Josephs, S.F.; Ratner, L.; Clarke, M.F.; Westin, E.H.; Reitz, M.S.; Wong-Staal, F.
 Science 225, 636-639, 1984
 A:Title: Transforming potential of human c-sis nucleotide sequences encoding platelet-de
 A:Reference number: A94276; MUID:84250225
 A:Accession: A94276
 A:Molecule type: DNA
 A:Residues: 1-241 <JOS1>
 A:Cross-references: GB:K01401; NID:G338206; PIDN:AAA60552.1; PID:G338209
 R:Chiu, I.M.; Reddy, E.P.; Givol, D.; Robbins, K.C.; Tronick, S.R.; Aaronson, S.A.
 Cell 37, 123-129, 1984
 A:Title: Nucleotide sequence analysis identifies the human c-sis proto-oncogene as a str
 A:Reference number: A21024; MUID:84205633
 A:Accession: A21024
 A:Molecule type: DNA
 A:Residues: 17-20, 'RQ', '22-241 <CHT>
 A:Cross-references: GB:K01917; NID:G338197
 R:Proc, C.D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson, S.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 2392-2396, 1986
 A:Title: Structure and sequence of the human c-sis/platelet-derived growth factor 2 (SIS
 A:Reference number: A23532; MUID:86205961
 A:Accession: A23532
 A:Molecule type: mRNA
 A:Residues: 1-241 <RAO1>
 A:Cross-references: GB:M12783; GB:M16288; NID:G338210; PIDN:AAA60553.1; PID:G338211
 R:Collins, T.; Ginsburg, D.; Boss, J.M.; Orkin, S.H.; Pober, J.S.
 Nature 316, 748-750, 1985
 A:Title: Cultured human endothelial cells express platelet-derived growth factor B chain
 A:Reference number: A93366; MUID:85296313
 A:Accession: A93366
 A:Molecule type: mRNA
 A:Residues: 1-241 <COL>
 A:Cross-references: GB:X02811; NID:G35371; PIDN:CAA26579.1; PID:G35372
 R:Welch, H.A.; Seidat, W.; Schaiter, H.U.; Hoppe, J.
 FEBS Lett. 198, 344-348, 1986
 A:Title: The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which cod
 A:Reference number: A25141; MUID:86164981
 A:Accession: A25141
 A:Molecule type: mRNA
 A:Residues: 26-241 <WE1>
 A:Cross-references: GB:X03702; NID:G35374; PIDN:CAA27333.1; PID:G35375
 R:Antonlades, H.N.; Hunkapiller, M.W.
 Science 220, 963-965, 1983
 A:Title: Human platelet-derived growth factor (PDGF): amino-terminal amino acid sequence
 A:Reference number: A94271; MUID:83197379
 A:Accession: A94271
 A:Molecule type: Protein
 A:Residues: 82-100, 'E', '102-104, 'C', '106, 'C', '108-110 <AMT>
 R:Waterfield, M.D.; Scerace, G.T.; Whittle, N.; Stroobant, P.; Johansson, A.; Wasteson, A.
 Nature 304, 35-39, 1983
 A:Title: Platelet-derived growth factor is structurally related to the putative transfor
 A:Reference number: A93308; MUID:83245981
 A:Accession: A93308
 A:Molecule type: Protein
 A:Residues: 82-112 <WAT>
 R:Josephs, S.F.; Guo, C.; Ratner, L.; Wong-Staal, F.
 Science 223, 487-491, 1984
 A:Title: Human proto-oncogene nucleotide sequences corresponding to the transforming reg
 A:Accession: A43499; MUID:84097555
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA

A:Residues: 'Q', '22-241 <JOS2>
 R:Lu, K.V.; Rohde, M.F.; Thomason, A.R.; Kenney, W.C.; Lu, H.S.
 Biochem. J. 309, 411-417, 1995
 A:Title: Mistranslation of a TGA termination codon as tryptophan in recombinant plate
 A:Reference number: S56115; MUID:95351967
 A:Accession: S56115
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 82-93 <LUR>
 R:Rao, C.D.; Pech, M.; Robbins, K.C.; Aaronson, S.A.
 Mol. Cell. Biol. 8, 284-292, 1988
 A:Title: The 5' untranslated sequence of the c-sis/platelet-derived growth factor 2 t
 A:Reference number: 157635; MUID:88094398
 A:Accession: 157635
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-20 <RAO2>
 A:Cross-references: GB:M19719; NID:G189727; PIDN:AAA60349.1; PID:G553608
 R:Ratner, L.; Josephs, S.F.; Jarrett, R.; Reitz, M.S.
 Nucleic Acids Res. 13, 5007-5018, 1985
 A:Title: Nucleotide sequence of transforming human c-sis cDNA clones with homology to
 A:Reference number: 137266; MUID:85269623
 A:Accession: 137266
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-241 <RAO>
 A:Cross-references: EMBL:X02744; NID:G30246; PIDN:CAA26524.1; PID:G30247
 R:Johansson, A.; Heldin, C.H.; Wasteson, A.; Westermark, B.; Deuel, T.F.; Huang, J.S.;
 EMBO J. 3, 921-928, 1984
 A:Title: The c-sis gene encodes a precursor of the B chain of platelet-derived growth
 A:Reference number: A55030; MUID:84236121
 A:Accession: A55030
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 'T', 'SL', '17-20, 'RQ', '22-241 <JOH>
 A:Cross-references: GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562
 R:Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
 Nucleic Acids Res. 23, 2815-2822, 1995
 A:Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis int
 A:Reference number: S58382; MUID:95388493
 A:Accession: S58383
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'M', '22-200 <DIR>
 A:Cross-references: EMBL:X83705; NID:G951023; PIDN:CAA58679.1; PID:G951025
 R:Cook, A.L.; Kirwin, P.M.; Craig, S.; Bawden, L.J.; Green, D.R.; Price, M.J.; Richar
 Biochem. J. 281, 57-65, 1992
 A:Title: Purification and analysis of proteinase-resistant mutants of recombinant pla
 A:Reference number: 138108; MUID:92117992
 A:Accession: 138108
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 'M', '82-241 <COO>
 A:Cross-references: EMBL:X65966; NID:G311378; PIDN:CAA5383.1; PID:G35377
 A:Note: mutagenized recombinant sequence
 C:Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal
 C:Genetics:
 A:Gene: GDB:PDGFB
 A:Cross-references: GDB:120709; OMIM:190040
 A:Map position: 22q12.3-22q13.1
 A:Introns: 57/3; 241/1; 192/3; 241/1
 C:Complex: homodimer; heterodimer (see PIR:PFHUG1)
 C:Superfamily: platelet-derived growth factor
 C:Keywords: growth factor; mitogen
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-81/Domain: amino-terminal propeptide #status predicted <PRO>
 F:82-190/Product: platelet-derived growth factor chain B #status experimental <MAT>
 F:155-163/Region: receptor binding #status predicted
 F:191-241/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:97-141, 130-178, 134-180/Disulfide bonds: #status experimental
 F:124/Disulfide bonds: Interchain (to 133 in homodimeric form) #status experimental
 F:133/Disulfide bonds: Interchain (to 124 in homodimeric form) #status experimental

S25097
platelet-derived growth factor chain B precursor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S25097; S33765; 152866
R:Herrén, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
submitted to the EMBL Data Library, July 1992
A:Description: Cross-species conservation in sequence and function of PDGF ligands and r
A:Reference number: S25096.
A:Accession: S25097
A:Molecule type: mRNA
A:Residues: 1-225 <HER1>
A:Cross-references: EMBL:Z14117; NID:g56867; PIDN:CA78487.1; PID:g56868
R:Herrén, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
Biochim. Biophys. Acta 1173, 294-302, 1993
A:Title: Conservation in sequence and affinity of human and rodent PDGF ligands and rece
A:Reference number: S33764; MUID:93305723
A:Accession: S33765
A:Molecule type: mRNA
A:Residues: 89-172 <HER2>
A:Cross-references: EMBL:Z14117
R:Lindner, V.; Giacchetti, C.M.; Schwartz, S.M.; Reidy, M.A.
Circ. Res. 76, 951-957, 1995
A:Title: A subpopulation of smooth muscle cells in injured rat arteries expresses plate
A:Reference number: 152866; MUID:95277908
A:Accession: 152866
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 74-182 <RES>
A:Cross-references: GB:L40991; NID:g727177; PIDN:AAA70048.1; PID:g727178
C:Genetics:
A:Gene: PDGF-B
C:Superfamily: platelet-derived growth factor
C:Keywords: growth factor; mitogen; platelet

Query Match 15.9%; Score 114.5; DB 2; Length 225;
Best Local Similarity 32.0%; Pred. No. 0.00082;
Matches 32; Conservative 19; Mismatches 33; Indels 17; Gaps 5;

Qy 45 ATCCPREVVPPLTVELMG-TVAKOLV-PSCVTVORCGGCCPPDGLCEVPTGHOVMOITL 102
| | | | | : | | | | | | | | | | | : | | : | | : |
Db 87 AECKRTVEFQISRLNIDRTNANFLWMPCEVQRCGCCNNRNVQCRAS---QVQMRPV 143
| | | | | : | | | | | | | | | | | : | | : | | : |

Qy 103 MIR-----YPSQLGEMSLSEHSQCECRPKKDSAYK 135
| | | | | : | | | | | | | | | | | : | | : | | : |
Db 144 QVRKIEIVRKRPFKKATVTLDDHLCRC----ETVYVP 178
| | | | | : | | | | | | | | | | | : | | : | | : |

RESULT 31
PFMSGB
platelet-derived growth factor chain B precursor (sis) - mouse
N:Alternate names: PDGF-related transforming protein
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1992 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C:Accession: A39073
R:Bonthron, D.T.; Sultan, P.; Collins, T.
Genomics 10, 287-292, 1991
A:Title: Structure of the murine c-sis proto-oncogene (Sis, PDGFB) encoding the B chain
A:Reference number: A39073; MUID:91257844
A:Accession: A39073
A:Molecule type: DNA
A:Residues: 1-241 <BON>
A:Cross-references: GB:M64849; GB:M55394; NID:g192818; PIDN:AAA37485.1; PID:g192820
C:Genetics:
A:Gene: sis
C:Superfamily: platelet-derived growth factor
C:Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-81/Domain: propeptide #status predicted <PRO>
F:82-190/Product: platelet-derived growth factor chain B #status predicted <MAT>
F:159-163/Region: receptor binding #status predicted
F:63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.9%; Score 114; DB 1; Length 241;
Best Local Similarity 33.7%; Pred. No. 0.00098;
Matches 30; Conservative 17; Mismatches 30; Indels 12; Gaps 4;

Qy 45 ATCCPREVVPPLTVELMG-TVAKOLV-PSCVTVORCGGCCPPDGLCEVPTGHOVMOITL 102
| | | | | : | | | | | | | | | | | : | | : | | : |
Db 95 AECKRTVEFQISRLNIDRTNANFLWMPCEVQRCGCCNNRNVQCRAS---QVQMRPV 151
| | | | | : | | | | | | | | | | | : | | : | | : |

Qy 103 MIR-----YPSQLGEMSLSEHSQCEC 124
| | | | | : | | | | | | | | | | | : | | : | | : |
Db 152 QVRKIEIVRKRPFKKATVTLDDHLCRC 180
| | | | | : | | | | | | | | | | | : | | : | | : |

RESULT 32
A25669
PDGF-related transforming protein (v-sis) - simian sarcoma virus
C:Species: simian sarcoma virus
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 12-Apr-1995
C:Accession: A25669
R:Hannink, M.; Sauer, M.K.; Donoghue, D.J.
Mol. Cell. Biol. 6, 1304-1314, 1986
A:Reference number: A25669; MUID:87064399
A:Accession: A25669
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-271 <HAN>
A:Note: deletions in the C-terminal Coding Region of the v-sis Gene: Dimerization is
C:Superfamily: platelet-derived growth factor

Query Match 15.4%; Score 111; DB 2; Length 271;
Best Local Similarity 33.7%; Pred. No. 0.0021;
Matches 30; Conservative 17; Mismatches 30; Indels 12; Gaps 4;

Qy 45 ATCCPREVVPPLTVELMG-TVAKOLV-PSCVTVORCGGCCPPDGLCEVPTGHOVMOITL 102
| | | | | : | | | | | | | | | | | : | | : | | : |
Db 125 AECKRTVEGEISRLNIDRTNANFLWMPCEVQRCGCCNNRNVQCRPT---QVQMRPV 181
| | | | | : | | | | | | | | | | | : | | : | | : |

Qy 103 MIR-----YPSQLGEMSLSEHSQCEC 124
| | | | | : | | | | | | | | | | | : | | : | | : |
Db 182 QVRKIEIVRKRPFKKATVTLDDHLCRC 210
| | | | | : | | | | | | | | | | | : | | : | | : |

RESULT 33
JC7592
spinal cord-derived growth factor-B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C:Accession: JC7592
R:Hamada, T.; Ue-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Contents: Fetal brain
A:Accession: JC7592
A:Molecule type: mRNA
A:Residues: 1-370 <HAM>
A:Cross-references: DBJ:AB052170
C:Genetics:
A:Gene: scdgf-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial 9
F:294-308/Region: conserved motif #status predicted

Query Match 13.3%; Score 95.5; DB 2; Length 370;
Best Local Similarity 27.9%; Pred. No. 0.092;
Matches 34; Conservative 18; Mismatches 43; Indels 27; Gaps 6;


```

Query Match      10.6%; Score 76; DB 2; Length 452;
Best Local Similarity 21.8%; Pred. No. 8.7;
Matches 22; Conservative 22; Mismatches 33; Indels 24; Gaps 4;

OY 23 VSQDAPGHQKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCTVORCGGC 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 LSGKMGKGNRERLASFND-----KVRQGSYPCS-----TCPMLPVCGGSC 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 83 PD---DGLECVPTGQHOVRRMQLMIRPSSQLGEMSLSEHS 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 PKSWLEGEIEPCSAKHNI-ORLLTYALSRIEREAANOEA 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 38
T31560
hypothetical protein Y105C5A.c - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C:Accession: T31560
R:McMurray, A.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21045
A:Accession: T31560
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <WIL>
A:Cross-references: EMBL:AL117193; PIDN:CAB54983.1; CESP:Y105C5A.c
A:Experimental source: clone Y105C5A
C:Genetics:
A:Gene: CESP:Y105C5A.c
A:Introns: 18/3
C:Superfamily: gliadin

Query Match      10.5%; Score 75.5; DB 2; Length 335;
Best Local Similarity 23.7%; Pred. No. 7.4;
Matches 27; Conservative 18; Mismatches 58; Indels 11; Gaps 3;

OY 26 PDAGHQRKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCTVORCGG 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 PVAPAPVQCPCSCMPVCEQSVAPAPVYISLNLEVPQCQCCAPCCQCPAQCQCCON 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 81 CCPDGLCECVPTGQHOVRRMQLMIRPSSQLGEMSLSEHSQC--ECRPRKKDSA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TCQ----QYAPVCCQCCAPCQCTFPSPAPACQCCQCTQCCQCCQCTPCCQCPA 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 39
AG0273
probable iron-sulfur protein YP02245 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0273
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0273
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC91051.1; PID:g15980245; GSPDB:GN00175
C:Genetics:
A:Gene: YP02245
C:Superfamily: conserved hypothetical protein H11684; ferredoxin 2[4Fe-4S] homology

Query Match      10.4%; Score 75; DB 2; Length 188;
Best Local Similarity 27.8%; Pred. No. 4.8;
Matches 25; Conservative 13; Mismatches 40; Indels 12; Gaps 4;

```

```

OY 8 LILAAIOLAPQAQPVSDPAGHQRKRVSWIDYTRATCQ-----PREVVPLTVELM 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 LKIAELLAVEP--QPLDDESAHQKRVAFIDENICIGCTKICIOACVDAITGAT-RAM 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 62 GTVAKOLVPSCTVORCGGCPDDGLECV 91
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 HTVLSDLCTGC---DLVAPCPPTDCIEMIP 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 40
T31559
hypothetical protein Y105C5A.b - Caenorhabditis elegans
N:Alternate names: Y105C5A.e
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C:Accession: T31559; T31562
R:McMurray, A.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21045
A:Accession: T31559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <WIL>
A:Cross-references: EMBL:AL117193; PIDN:CAB54982.1; CESP:Y105C5A.b
A:Experimental source: clone Y105C5A
A:Accession: T31562
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-335 <WIL>
A:Cross-references: EMBL:AL117193; PIDN:CAB54985.1; CESP:Y105C5A.e
A:Experimental source: clone Y105C5A
C:Genetics:
A:Gene: CESP:Y105C5A.b; CESP:Y105C5A.e
A:Introns: 18/3
C:Superfamily: gliadin

Query Match      10.4%; Score 75; DB 2; Length 335;
Best Local Similarity 24.4%; Pred. No. 8.3;
Matches 30; Conservative 18; Mismatches 51; Indels 24; Gaps 6;

OY 19 AQAAPV-PPDA-PGHQRKRVSWIDYTRATCQPREVVPLTVELMGTVAKOLVPSCTVORCGG 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 APAPVQCPCSCMPVCEQSVAPAPVYISLNLEVPQCQCCAPCCQCPAQCQCCQPS 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 73 -VTVORCGGCPDDGLECVPTGQHOVRRMQLMIRPSSQLGEMSLSEHSQC--ECRPRKK 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 APQCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 130 DSA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 QPA 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 41
T31840
hypothetical protein T05B4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31840
R:Bradshaw, H.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid T05B4.
A:Reference number: Z21092
A:Accession: T31840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-293 <BR>
A:Cross-references: EMBL:AF016445; PIDN:AAC69056.1; GSPDB:GN00023; CESP:T05B4.4
A:Experimental source: strain Bristol N2; clone T05B4
C:Genetics:
A:Gene: CESP:T05B4.4
A:Map position: 5

```

A;Gelle: 2604.1

C;Accession: J21/85; J21/91

C:\Accession: T21785: T21791
C:\Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000

R;Gardner, A.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19472
 A;Accession: T21785
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-249 <full>
 A;Cross-references: EMBL:Z81529; PIDN:CAB04291.1; GSPDB:GN00023; CESP:F35E8.10
 A;Experimental source: clone F35E8
 A;Accession: T21791
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-249 <full>
 A;Cross-references: EMBL:Z81529; PIDN:CAB04297.1; GSPDB:GN00023; CESP:F35E8.13
 A;Experimental source: clone F35E8
 C;Genetics:
 A;Gene: CESP:F35E8.10; CESP:F35E8.13
 A;Map position: 5
 A;Intons: 33/3; 121/1
 C;Superfamily: Caenorhabditis elegans hypothetical protein C49G7.3

Query Match 10.1%; Score 72.5; DB 2; Length 249;
 Best Local Similarity 27.5%; Pred. No. 11;
 Matches 28; Conservative 8; Mismatches 41; Indels 25; Gaps 5;
 QY 21 APVSGPDAFGHQRKVSMDVYTRATCOPREVVPLIYELMGTVAKOLVPSCTVYQRCGG 80
 |||: | | | : || | | | : | | : | |
 Db 58 APVADGVPSPGRDQGRPLACTYATATPAV-----VQDKRNAAQSTCP-----RTGGL 107
 QY 81 CCPDGLGCVPTGQHGVNMQILMIRYPSQSGEKSLSEHSOC 122
 || | | | | | : | | | : | |
 Db 108 CCQTSGYNC-PN-----VAIPRLNCGTITA---SOC 134

Search completed: September 10, 2002, 02:51:08
 Job time: 3576 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 02:49:22 ; Search time 24.95 seconds
(without alignments)
211.056 Million cell updates/sec

Title: US-09-912-436-6
Perfect score: 719
Sequence: 1 MSPILRLRLAALLQLAPAQ.....EHSQCCECPKPKDSAVKPD 136

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105223

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 99%
Listing first 45 summaries

Database : SwissProt-40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688	95.7	207	1	VEGH_BOVIN
2	644	89.6	207	1	VEGH_MOUSE
3	521	72.5	135	1	VEGH_RAT
4	275.5	38.3	190	1	VEGA_HORSE
5	270.5	37.6	190	1	VEGA_PIG
6	269.5	37.5	190	1	VEGA_MESAU
7	269.5	37.5	214	1	VEGA_RAT
8	268.5	37.3	214	1	VEGA_CANFA
9	267.5	37.2	214	1	VEGA_MOUSE
10	266.5	37.1	190	1	VEGA_BOVIN
11	264	36.7	232	1	VEGA_HUMAN
12	263.5	36.6	146	1	VEGA_SHEEP
13	254.5	35.4	164	1	VEGA_CAVPO
14	236	32.8	216	1	VEGA_CHICK
15	199.5	27.7	133	1	VEGH_ORFEN2
16	181.5	25.2	149	1	PLGF_BOVIN
17	176.5	24.5	221	1	PLGF_HUMAN
18	176	24.5	158	1	PLGF_MOUSE
19	176	24.5	158	1	PLGF_MOUSE
20	155.5	21.6	358	1	VEGD_MOUSE
21	149.5	20.8	326	1	VEGD_RAT
22	147	20.4	354	1	VEGD_MOUSE
23	146.5	20.4	354	1	VEGD_MOUSE
24	145.5	20.2	148	1	VEGH_ORF7
25	145	20.2	419	1	VEGH_HUMAN
26	129	17.9	211	1	PDGA_HUMAN
27	127.5	17.7	213	1	PDGA_HUMAN
28	127	17.7	204	1	PDGA_RAT
29	127	17.7	211	1	PDGA_MOUSE
30	127	17.7	245	1	PDGB_FELCA
31	123	17.1	226	1	TSIS_SMSAV
32	123	17.1	241	1	PDGB_HOMO
33	119	16.6	226	1	PDGA_XENLA

34	114.5	15.9	225	1	PDGB_RAT	Q05028	rattus norv
35	114	15.9	241	1	PDGB_MOUSE	P31240	mus muscu
36	108	15.0	241	1	PDGB_SHEEP	O95229	ovis aries
37	104.5	14.5	126	1	VEGC_RAT	O35757	rattus norv
38	78	10.8	378	1	DNJ2_MYCLE	O49762	mycobacteri
39	73.5	10.2	1416	1	YNB1_CAEEL	Q03610	caenorhabdi
40	72.5	10.1	591	1	GRN_CAVPO	P28797	cavia porce
41	72.5	10.1	1064	1	CY4A_RAT	P26770	rattus norv
42	72.5	10.1	1097	1	CC1_DROME	O96433	drosophila
43	72	10.0	356	1	HXB2_HUMAN	P14652	homo sapien
44	71	9.9	751	1	SM3C_MOUSE	O62181	mus muscu
45	70.5	9.8	550	1	YL00_MYCTU	Q10709	mycobacteri

ALIGNMENTS

```

RESULT 1
VEGH_BOVIN STANDARD: PRT; 207 AA.
AC 09XS49: 09XS48: 09GLX2:
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related
DE factor) (VRF).
GN VEGFB OR VRF.
OS Bos taurus (Bovine).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Cetiartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 38-104 FROM N.A.
RC TISSUE=Heart;
RA Mandriota S.J., Pepper M.S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
CC heparin and neuropilin-1 whereas the binding to neuropilin-1 of
CC VEGF-B186 is regulated by proteolysis (By similarity).
CC - SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
CC with vegf (By similarity).
CC - SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity).
CC - ALTERNATIVE PRODUCTS: At least 2 isoforms: VEGF-B186 (shown here)
CC and VEGF-B167; are produced by alternative splicing.
CC - PTM: VEGF-B167 is O-glycosylated (By similarity).
CC - SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
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DR EMBL; AB004273; BAA77686.1; -
DR EMBL; AB004273; BAA77685.1; -
DR EMBL; AF099134; AAC29746.1; -
DR HSSP; P15692; 1VP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.

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QY	61	MGYAKOVLPCVCVYQVRGCGCCPDGGLCEVPTGQHOVMQILMIRYPSPOLGEMSLIEHS	120
Db	61	MGNYKOLVLPSCVYVQRCGCCCPDGLCEVPTGQHOVMQILMIOYPSPOLGEMSLIEHS	120
QY	121	QCECRPKRKSDAVNPD	136
Db	121	QCECRPKRKESAVNPD	136
RESULT	3		
VEGB_RAT	STANDARD;	PRT;	135 AA.
ID	AC	035485; 054881;	
DT	01-MAR-2002	(Rel. 41, Created)	
DT	01-MAR-2002	(Rel. 41, Last sequence update)	
DT	01-MAR-2002	(Rel. 41, Last annotation update)	
DE	Vascular endothelial growth factor B (VEGF-B) (VEGF related factor)		
DE	(VRE) (Fragment).		
GN	VEGFB OR VRF.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORM VEGF-B186).		
RA	Strain=Sprague-Dawley; TISSUE=Placenta;		
RL	Mandriota S.J., Pepper M.S.;		
RL	Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORM VEGF-B167).		
RA	TISSUE=Heart;		
RA	Well J., Eschenhagen T., Mittleman C., Scholz H.;		
RL	Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.		
CC	-1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds		
CC	heparin and neuropilin-1 whereas the binding to neuropilin-1 of		
CC	VEGF-B186 is regulated by proteolysis (By similarity).		
CC	-1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer		
CC	with vegf (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or		
CC	to the extracellular matrix unless released by heparin (By		
CC	similarity).		
CC	-1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)		
CC	and VEGF-B167; are produced by alternative splicing.		
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.		
CC			
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF032925; AAB68884.1; -		
DR	EMBL; AF022952; AAB95447.1; -		
DR	HSSP; P15692; IVP.		
DR	Interpro; IPR000072; PDGF.		
DR	Pfam; PF00341; PDGF_1.		
DR	Prodom; PD001629; PDGF_1.		
DR	SMART; SM00141; PDGF_1.		
DR	PROSITE; PS00249; PDGF_1; 1.		
DR	PROSITE; PS0278; PDGF_2; 1.		
KW	Mitogen; Growth factor; Heparin-binding; Alternative splicing;		
KW	Multigene family.		
FT	NON_TER	1	
FT	DISULFID	47	91
FT	DISULFID	51	93
FT	DISULFID	41	41
FT	DISULFID	50	50
FT	VARSPLIC	106	>135
FT			
FT	CONFLICT	29	29

FT	CONFLICT	37	37	L -> F (IN REF. 2).
FT	CONFLICT	98	98	R -> K (IN REF. 2).
FT	NON_TER	135	135	
SO	SEQUENCE	135 AA;	15001 MW;	A915863D8586F82D CRC64;
	Query Match	72.5%;	Score 521;	DB 1;
	Best Local Similarity	89.5%;	Pred. No. 9.3e-47;	Length 135;
	Matches 94;	Conservative	7;	Mismatches 4;
			Indels	0;
			Gaps	0;
Oy	32	ORKVSWIDVYTRATCGREVVVPLTVLMLGTVAKVLPGSCVTYVRCGGCCPDGLEGCP	91	
Db	1	KRKVSWIDVYARATCGREVVVPLTMLMGVNVKQLVPCVTYVRCGGCCPDGLEGCP	60	
Oy	92	TGQHOVRMQLIMIRYPSQLGEMSLSEHSQCECRPKKDSAVKPD	136	
Db	61	IGOHVRMQLIMIRYPSQLGEMSLSEHSQCECRPKKRESAVKPD	105	
RESULT	4			
VEGA_HORSE	STANDARD;	PRT;	190 AA.	
ID	VEGA_HORSE			
AC	09GKR0;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular			
DE	permeability factor) (VPF).			
GN	VEGF OR VEGFA.			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RA	Miura N., Miura K., Kawahara K., Nakashima M., Fukunitsu S.,			
RA	Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;			
RT	"Cloning of cDNA and high-level expression of equine vascular			
RT	endothelial growth factor (VEGF)."			
RL	Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: Growth factor active in angiogenesis, and endothelial			
CC	cell growth. Induces endothelial proliferation and vascular			
CC	permeability (by similarity).			
CC	-1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer			
CC	with p1GF (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or			
CC	to the extracellular matrix unless released by heparin (By			
CC	similarity).			
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC				
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CC	use by non-profit institutions as long as its content is in no way			
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CC				
DR	EMBL: AB053350: BAB0890.1; -			
DR	InterPro: IPR000072; PDGF.			
DR	Pfam: PF00341; PDGF; 1.			
DR	ProDom: PD001629; PDGF; 1.			
DR	SMART: SM00141; PDGF; 1.			
DR	PROSITE: PS00249; PDGF_1; 1.			
DR	PROSITE: PS00278; PDGF_2; 1.			
KW	Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;			
KW	Multigene family.			
FT	SIGNAL	1	26	POTENTIAL.
FT	CHAIN	27	190	VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT	DISULFID	51	93	BY SIMILARITY.
FT	DISULFID	82	127	BY SIMILARITY.
FT	DISULFID	86	129	BY SIMILARITY.
FT	DISULFID	76	76	INTERCHAIN (BY SIMILARITY).

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF063013; AAK00049.1; -
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF; 1.
 DR ProDom: PD001629; PDGF; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS00278; PDGF_2; 1.
 KW Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
 KW Heparin-binding; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 190
 FT DISULFID 51 93
 FT DISULFID 82 127
 FT DISULFID 86 129
 FT DISULFID 76 76
 FT DISULFID 85 85
 FT CARBOHYD 100 100
 SQ SEQUENCE 190 AA: 22276 MW: F00C5A8EA79A465F CRC64;

Query Match 37.5%; Score 269.5; DB 1; Length 190;
 Best Local Similarity 44.3%; Pred. No. 9.3e-21;
 Matches 54; Conservative 20; Mismatches 45; Indels 3; Gaps 2;

OY 10 LALLLQAPAPAVSPDAPGHOHK--VSMIVYVTRATCPREVVPLVLELMTGATKQ 67
 DB 12 LALLLTLHNAKMSQAPRTTEBOKAHCYVEFMVYRKYCHPIETLVDTQETPDELEYI 71
 OY 68 LVPSCVTORCGCCGDDGLECVPGOHVMOILMR-YPSQLGMSLEHSQCRCR 126
 DB 72 FKPSCVPLMRGCGCSDEALECVPTSESNTTQIMRVKPHQSHIGMSFLQHSRCRCR 131
 OY 127 KK 128
 DB 132 KK 133

RESULT 7
 VEGA_RAT STANDARD; PRT; 214 AA.
 AC P16612; Q9QXG7; Q9QXG6; Q9QXK7;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 DE permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_Taxid=10116;
 RX MEDLINE=90207249; PubMed=2320579;
 RA Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
 RA Pallis T.M., Hope D.A., Thomas K.A.;
 RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
 RT that is homologous to platelet-derived growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190.
 RX MEDLINE=90207249; PubMed=2320579;
 RA Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
 RA Pallis T.M., Hope D.A., Thomas K.A.;
 RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
 RT that is homologous to platelet-derived growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-A188; VEGF-A164; VEGF-A144 AND
 RP VEGF-A120).
 RA Ishii H., Arakawa T., Okayama M., Oota I., Takuma T., Inomata K.;
 RT "Developmental expression of vascular endothelial growth factor-A
 RT (VEGF-A) splicing variants, VEGF-A188, VEGF-A164, and VEGF-A120 in rat
 RT mesenter muscle.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE OF 27-40.
 RC TISSUE=Glial tumor;
 RX MEDLINE=95221439; PubMed=7706320;
 RA D'Salvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,
 RA Siderman D.D., Pallis T.M., Sullivan K.A., Thomas K.A.;
 RT "Purification and characterization of a naturally occurring vascular
 RT endothelial growth factor/placenta growth factor heterodimer.";
 RL J. Biol. Chem. 270:7717-7723(1995).
 CC - FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
 CC endothelial cell growth. It induces endothelial cell
 CC proliferation, promotes cell migration, inhibits apoptosis, and
 CC induces permeabilization of blood vessels. It binds to the
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
 CC heparin (By similarity).
 CC - SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with PlGF (By similarity).
 CC - SUBCELLULAR LOCATION: VEGF-A120 is acidic and freely secreted.
 CC VEGF-A164 is more basic, has heparin-binding properties and,
 CC although a significant proportion remains cell-associated, most is
 CC freely secreted. VEGF-A188 is very basic; it is cell-associated
 CC after secretion and is bound avidly by heparin and the
 CC extracellular matrix, although it may be released as a soluble
 CC form by heparin, heparinase or plasmin (By similarity).
 CC - ALTERNATIVE PRODUCTS: At least 4 isoforms: VEGF-A188 (shown here),
 CC VEGF-A164, VEGF-A144 and VEGF-A120; are produced by alternative
 CC splicing.
 CC - TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in
 CC particularly in supraoptic and paraventricular nuclei and the
 CC choroid plexus. Also found abundantly in the corpus luteum of
 CC the ovary and in kidney glomeruli.
 CC - SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC
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DR EMBL: M32167; AAA41211.1; -
 DR EMBL: AF215725; AAF19211.1; -
 DR EMBL: AF215726; AAF19212.1; -
 DR EMBL: AF222779; AAF25958.1; -
 DR PIR: A35987; A35987.
 DR HSP: P15692; IVP.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF; 1.
 DR ProDom: PD001629; PDGF; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS00278; PDGF_2; 1.
 KW Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
 KW Heparin-binding; Alternative splicing; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 214
 FT DISULFID 51 93
 FT DISULFID 82 127
 FT DISULFID 86 129
 FT DISULFID 76 76
 FT DISULFID 85 85
 FT CARBOHYD 100 100
 FT VARSPLIC 140 140
 FT VARSPLIC 141 141
 FT VARSPLIC 141 164
 FT VARSPLIC 141 208
 FT VARSPLIC 165 208
 FT CONFLICT 101 101
 FT CONFLICT 101 101
 SQ SEQUENCE 214 AA: 25239 MW: 60FBB876F5304946 CRC64;

Query Match 37.5%; Score 269.5; DB 1; Length 214;
 Best Local Similarity 43.8%; Pred. No. 1.1e-20;


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RL J. Biol. Chem. 271:3877-3883(1996).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (by similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (by similarity).
CC -1- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3
CC remains cell-surface associated unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; VEGF-3/VEGF188 (shown here),
CC VEGF-1/VEGF164 and VEGF-2/VEGF120; are produced by alternative
CC splicing.
CC -1- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the
CC choroid plexus, paraventricular neuroepithelium, placenta and
CC kidney glomeruli. Also found in bronchial epithelium, adrenal
CC gland and in seminiferous tubules of testis. High expression of
CC VEGF continues in kidney glomeruli and choroid plexus in adults.
CC -1- DOMAIN: VEGF-3 contains a basic insert which acts as a cell
CC retention signal.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL: S37052; AAB22252.1; -
DR EMBL: S38083; AAB22253.1; -
DR EMBL: S38100; AAB22254.1; -
DR EMBL: M95200; AAA40347.1; -
DR EMBL: U41383; -; NOT_ANNOTATED_CDS.
DR PIR: A43351; A43351.
DR HSSP: P15692; 2VPE.
DR MGD: MGI:103178; Vegf.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Angiogenesis; Growth factor; Multigene family.
FT SIGNAL 1 26
FT CHAIN 1 214
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
FT VARSPLIC 140 140
FT VARSPLIC 141 164
FT VARSPLIC 141 208
FT CONFLICT 117 118
SQ SEQUENCE 214 AA; 25283 MW; B540B51E4BB6B17 CRC64;

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Query Match 37.2%; Score 267.5; DB 1; Length 214;
 Best Local Similarity 42.3%; Pred. No. 1.7e-20;
 Matches 55; Conservative 23; Mismatches 47; Indels 5; Gaps 3;

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OY 127 KKKDSAVKPD 136
DB 132 KK--DRTKPE 139

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RESULT 10
 VEGA_BOVIN
 ID VEGA_BOVIN STANDARD; PRT; 190 AA.
 AC P15691;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
 DE permeability factor) (VPF).
 GN VEGF OR VEGFA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OX
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
 RX MEDLINE=90069608; PubMed=2479986;
 RA Leung D.W., Cachianes G., Kiang W.-J., Goeddel D.V., Ferrara N.,
 RT "Vascular endothelial growth factor: a new member of the platelet-
 RT derived growth factor gene family";
 RL Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
 RN [3]
 RP SEQUENCE OF 27-31.
 RA MEDLINE=89286596; PubMed=2735925;
 RX Ferrara N., Henzel W.J.,
 RT "Pituitary follicular cells secrete a novel heparin-binding growth
 RT factor specific for vascular endothelial cells";
 RL Biochem. Biophys. Res. Commun. 161:851-858(1989).
 CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
 CC endothelial cell growth. It induces endothelial cell
 CC proliferation, promotes cell migration, inhibits apoptosis, and
 CC induces permeabilization of blood vessels. It binds to the
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
 CC heparin (by similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
 CC with PlGF (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 CC to the extracellular matrix unless released by heparin (by
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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 CC -----
 DR EMBL: M32976; AAA30502.1; -
 DR EMBL: M31836; AAA30804.1; -
 DR EMBL: M33750; AAA30805.1; -
 DR PIR: A33255; A33255.
 DR PIR: A33787; A33787.
 DR PIR: B40080; B40080.
 DR HSSP: P15692; 1VGH.

RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [14]
RP PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE=90062112; PubMed=2584205;
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA Siegel N., Haymore B.L., Lelmgubner R., Feder J.;
RT "human vascular permeability factor. Isolation from U937 cells.";
RL J. Biol. Chem. 264:20017-20024(1989).
RN [15]
RP SEQUENCE OF 27-41.
RX MEDLINE=93145946; PubMed=7678805;
RA Fieblisch B.L., Jaeger B., Schoellmann C., Weindel K., Wiltling J.,
RA Kochs G., Marne D., Hug H., Welch H.A.;
RT "synthesis and assembly of functionally active human vascular
permeability factor homodimers in insect cells.";
RL Eur. J. Biochem. 211:19-26(1993).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX MEDLINE=97352774; PubMed=9207067;
RA Muller Y.A., Li B., Christlinger H.W., Wells J.A., Cunningham B.C.,
RA de Vos A.M.;
RT "vascular endothelial growth factor: crystal structure and functional
mapping of the kinase domain receptor binding site";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE=98035455; PubMed=9351807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT "the crystal structure of vascular endothelial growth factor (VEGF)
refined to 1.93-A resolution: multiple copy flexibility and receptor
binding.";
RL Structure 5:1325-1338(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE=99119204; PubMed=9922142;
RA Wiseman C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT "crystal structure of the complex between VEGF and a receptor-blocking
peptide.";
RL Biochemistry 37:17765-17772(1998).
RN [19]
RP STRUCTURE BY NMR OF 34-135.
RX MEDLINE=97477915; PubMed=9336848;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "1H, 13C, and 15N backbone assignment and secondary structure of the
receptor-binding domain of vascular endothelial growth factor";
RL protein sci. 6:2250-2260(1997).
RN [20]
RP STRUCTURE BY NMR OF 137-215.
RX MEDLINE=98298440; PubMed=9654701;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "solution structure of the heparin-binding domain of vascular
endothelial growth factor.";
RL structure 6:637-648(1998).
RN [21]
RP FUNCTION.
RX MEDLINE=21320570; PubMed=11427521;
RA Murphy J.F., Fitzgerald D.J.;
RT "vascular endothelial growth factor induces cyclooxygenase-dependent
proliferation of endothelial cells via the VEGF-2 receptor.";
RL FASEB J. 15:1667-1669(2001).
RN [22]
RP FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
endothelial cell growth. It induces endothelial cell
proliferation, promotes cell migration, inhibits apoptosis, and
induces permeabilization of blood vessels. It binds to the
VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.
CC -1 SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
with PlGF (By similarity).

```

CC      -I- SUBUNIT: LOCATION: VEGF121 is acidic and freely secreted.
CC      VEGF165 is more basic, has heparin-binding properties and,
CC      although a significant proportion remains cell-associated, most is
CC      freely secreted. VEGF189 is very basic; it is cell-associated
CC      after secretion and is bound avidly by heparin and the
CC      extracellular matrix, although it may be released as a soluble
CC      form by heparin, heparinase or plasmin.
CC      -I- ALTERNATIVE PRODUCTS: 7 isoforms, VEGF206 (shown here), VEGF189,
CC      VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be
CC      produced by alternative splicing.
CC      -I- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms
CC      are widely expressed, whereas the VEGF206 and VEGF-145 are
CC      uncommon.
CC      -I- INDUCTION: Regulated by growth factors, cytokines, gonadotropins,
CC      nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.
CC      -I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC      -I- DATABASE: NAME=K&D Systems/ cytokine mini-reviews: VEGF;
CC      WWW="http://www.rndsystems.com/asp/g_steinbiller.asp?bodyId=230".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
CC      Query Match: 36.7%; Score 264; DB 1; Length 232;
CC      Best Local Similarity 43.9%; Pred. No. 4.2e-20;
CC      Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2
CC
CC      QY      10 LALLQLAPQAQPVASQDPAPG--HQKRVSNIDVYTRATCCPREVVVPLVETLNGTVAK 66
CC      Db      12 LALLLLHNHAKKSGAARPMAGGGGNHNEVVKRMADYGRGSCPIETFLVDIFQEDPELEY 71
CC      QY      67 QLVPSCVTVYQRCGGCCPRDDGLCEVPYRGCHQVNMQLMIR-YSSQLGEMSLSEHSQCECR 125
CC      Db      72 IFKPSCVPLMRGGCGNDEGLCEVPTEESNITMQLMRKHQGNHNGEMSFLLHNKCECR 131
CC      QY      126 PKK 128
CC      Db      132 PKK 134
CC
CC      RESULT 12
CC      VEGA_SHEEP STANDARD: PRT; 146 AA.
CC      AC      P50412:
CC      DT      01-OCT-1996 (Rel. 34, Created)
CC      DT      01-OCT-1996 (Rel. 34, Last sequence update)
CC      DF      01-MAR-2002 (Rel. 41, Last annotation update)
CC      DE      Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
CC      permeability factor) (VPF).
CC      GN      VEGF OR VEGFA.
CC      OS      Ovis aries (Sheep).
CC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC      OC      Bovidae; Caprinae; Ovis.
CC      NCBI_TaxID=9940;
CC      [1]
CC      RN      SEQUENCE FROM N.A.
CC      RP      TISSUE=Kidney;
CC      RX      MEDLINE=971117658; Pubmed=8958842;
CC      RA      Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
CC      RA      Reynolds L.P., Moor R.M.;
CC      RA      "Characterization and expression of vascular endothelial growth
CC      factor (VEGF) in the ovine corpus luteum.";
CC      RL      J. Reprod. Fertl. 108:157-165(1996).
CC      CC      -I- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC      endothelial cell growth. It induces endothelial cell
CC      proliferation, promotes cell migration, inhibits apoptosis, and
CC      induces permeabilization of blood vessels. It binds to the
CC      VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC      heparin (By similarity).
CC      CC      -I- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC      with PlGF (By similarity).
CC      CC      -I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC      CC      -----

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DR EMBL: X89506; LVP.1677.1; -
DR HSSP: P15692; IAPP.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Multigene family
FT SIGNAL 1 26
FT CHAIN 1 26
FT DISULFID 27 146
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
SQ SEQUENCE 146 AA; 17247 MW; 4E792CB57F91760 CRC64;

Query Match 36.6%; Score 263.5; DB 1; Length 146;
Best Local Similarity 44.3%; Pred. No. 3e-20;
Matches 54; Conservative 23; Mismatches 42; Indels 3; Gaps 2;

OY 10 LALLDLAPADVPDPADPHOR--KVYSMDVYTRATQPREVVVPLVFLMGTVAQ 67
DB 12 LALLDLIHAHAKQAPMAAGGQKREHVKFMVYQKSPFETLVDIQEYRDELFT 71
OY 63 LVSVCYVORCGCCPDGLEGVPTGQHOVMOILMIR-YPSQLGEMSLSEHSQCECRP 126
DB 72 FKPSCVPLMRGCGCNDSELECVPTSEFNITQIMRIKPHQSOHIGMSFLQHNKCECRP 131

OY 127 KK 128
DB 132 KK 133

RESULT 13

VEGA_CAVPO STANDARD: PRT; 164 AA.

AC P26617;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A (VEGF-A) (Vascular permeability
DE factor) (VPF).
GN VEGF OR VEGFA.

OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blle duct;

RA Berse B.;

RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: Growth factor active in angiogenesis, and endothelial

CC permeability (By similarity).

CC - SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer

CC with PlGF (By similarity).

CC - SUBCELLULAR LOCATION: Secreted but remains associated to cells or

CC to the extracellular matrix unless released by heparin (By

CC similarity).

CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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DR EMBL: M84230; AAA37057.1; -
DR HSSP: P15692; LVGH.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Mitogen: Angiogenesis; Growth factor; Glycoprotein.
KW Heparin-binding; Multigene family
FT SIGNAL 1 26
FT CHAIN 1 26
FT DISULFID 27 146
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
SQ SEQUENCE 164 AA; 19330 MW; 9EB86A19A9D5DC4A CRC64;

Query Match 35.4%; Score 254.5; DB 1; Length 164;
Best Local Similarity 45.8%; Pred. No. 2.8e-19;
Matches 49; Conservative 20; Mismatches 35; Indels 3; Gaps 2;

OY 26 PDAPHQ--RKVYSMDVYTRATQPREVVVPLVFLMGTVAQOLVPSCTVORCGCCP 83
DB 2 PMAGSGQKREBEVKFMFVYKRSYCRPIEMVYDFQYPRPEIEYIFKPSCVPLMRGCGCN 61
OY 84 DDLGECVPTGQHOVMOILMIR-YPSQLGEMSLSEHSQCECRPKK 129
DB 62 DESLECVPTSEFNITQIMRIKPHQSOHIGMSFLQHSKCECRPKE 108

RESULT 14

VEGA_CHICK STANDARD: PRT; 216 AA.

AC P52582; O91420;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.

OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031, 93934;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=Chicken; TISSUE=Heart;

RA Takahashi T.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: Growth factor active in angiogenesis, and endothelial

CC permeability (By similarity).

CC - SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer

CC with PlGF (By similarity).

CC - SUBCELLULAR LOCATION: Secreted but remains associated to cells or

CC to the extracellular matrix unless released by heparin (By

CC similarity).


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RP SEQUENCE OF 60-187 FROM N.A.
RC SPECIES=C.C.japonica;
RX MEDLINE=95301109; PubMed=7781909;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT differentiation in the quail embryo."
RL Dev. Biol. 169:699-712(1995).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Elt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms: VEGF190 (shown here),
CC VEGF166 and VEGF146; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Abundantly and equally expressed in heart and
CC liver. In kidney glomeruli, brain and yolk sac, VEGF166 is 5- to
CC 10-times more abundant than VEGF190.
CC -1- DEVELOPMENTAL STAGE: VEGF166 is expressed early at day 1 and is
CC upregulated during gastrulation. Expression of VEGF190 is detectable
CC only from day 2.
CC -1- DOMAIN: VEGF190 contains a basic insert which acts as a cell
CC retention signal.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB011078; BAA24925.1; -
DR EMBL: S79680; AAB35371.1; -
DR HSSP: P15692; 1VGH.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF.1.
DR ProDom: PD001629; PDGF.1.
DR SMART: SM00141; PDGF.1.
DR PROSITE: PS00249; PDGF.1.
DR PROSITE: PS0278; PDGF.2.1.
DR PROSITE: PS0278; PDGF.2.1.
DR Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT CHAIN 1 26
FT SIGNAL 1 26
FT CHAIN 27 216
FT DISULFID 52 94
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 130
FT DISULFID 77 77
FT DISULFID 86 86
FT CARBOHYD 101 101
FT VARSPLIC 142 142
FT VARSPLIC 143 166
FT VARSPLIC 166 166
FT VARSPLIC 167 210
SQ SEQUENCE 216 AA; 25203 MW; 82E669C2F6C6DA7 CRC64;

```

Query Match 32.8%; Score 236; DB 1; Length 216;
 Best Local Similarity 40.7%; Pred. No. 3e-17;
 Matches 50; Conservative 21; Mismatches 48; Indels 4; Gaps 2;

```

QY 10 LAALLQLAPAPVSPDAPGHRK---VVSMDVYTRATCPREVVPVPLTVELMGTYAK 66
DB 12 LAALLYLQSAELSKAALDGERKPNVYKLEVERSRFRTETLVDFQETPDEVEY 71
QY 67 QLVPSCTVORCGCGGCPDDGLECVPTGOHOVYRMOILMIR-YPSQSLGEMSLSEHSQECR 125
DB 72 IFRPSCVPLMKACGCCDEGLCEVPDVYVYNTMEIARIKPHOSQHIAHMSFLQHSKDCR 131

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QY 126 PKR 128
DB 132 PKR 134

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RESULT 15
 VEGF_ORFN2
 ID VEGF_ORFN2 STANDARD; PRT; 133 AA.
 AC P2584;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vascular endothelial growth factor homolog precursor.
 GN A2R.
 OS Orf virus (strain NZ2) (OV NZ-2).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Parapoxvirus.
 OX NCBI_TaxID=10259;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94076465; PubMed=8254780; S.B., Mercer A.A., Robinson A.J.;
 RA Lytle D.J., Fraser K.M., Fleming S.B.,
 RT "Homologs of vascular endothelial growth factor are encoded by the
 RT poxvirus orf virus."
 RT J. Virol. 68:84-92(1994).
 RL J. Virol. 68:84-92(1994).
 CC -1- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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 CC -----
DR EMBL: S67520; AAB29220.2; -
DR HSSP: P15692; 1VPP.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF.1.
DR ProDom: PD001629; PDGF.1.
DR SMART: SM00141; PDGF.1.
DR PROSITE: PS00249; PDGF.1.
DR PROSITE: PS0278; PDGF.2.1.
DR PROSITE: PS0278; PDGF.2.1.
DR Mitogen: Growth factor; Glycoprotein; Signal.
KW Heparin-binding; Alternative splicing; Multigene family.
FT CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 133
FT DISULFID 36 78
FT DISULFID 67 112
FT DISULFID 71 114
FT DISULFID 61 61
FT DISULFID 70 70
FT CARBOHYD 85 85
SQ SEQUENCE 133 AA; 14715 MW; 917C0F6883030C39 CRC64;

Query Match 27.7%; Score 199.5; DB 1; Length 133;
 Best Local Similarity 39.6%; Pred. No. 1e-13;
 Matches 36; Conservative 19; Mismatches 35; Indels 1; Gaps 1;

```

QY 38 MIDVYTRATCPREVVPVPLVELMGTYAKOLVPSCTVORCGCGCPDDGLECVPTGOHOV 97
DB 27 WSEVLKSGSECKPRPIVVPVSETHPELTSORENPPCVILMRGCGCNDSELCVPTBEVNV 86
QY 98 RMOILMIRYPSQ-YGEMSLSEHSQECRPRK 127
DB 87 SWEILGASGSGSGNGMORLSFVEHKKDCRPR 117

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RESULT 16

PLGF_BOVIN STANDARD: PRT: 149 AA.

ID PLGF_BOVIN 09X547;
 AC 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Placenta growth factor precursor (PLGF).
 GN PGF OR PLGF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
 RT "Structure and expression of bovine VEGF family.";
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
 CC -! FUNCTION: Growth factor active in angiogenesis, and endothelial
 CC cell growth, stimulating their proliferation and migration. It
 CC binds to receptor VEGFR-1/Flt1 (By similarity).
 CC -! SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
 CC heterodimer with VEGF/VEGF-A (By similarity).
 CC -! SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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 CC -----
 CC EMBL: AB004272; BAA77684.1; -.
 DR HSSP: P15692; 1VPP.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF; 1.
 DR ProDom: PD001629; PDGF; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS00278; PDGF_2; 1.
 KM Mitogen; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 149
 FT DISULFID 52 94
 FT DISULFID 83 128
 FT DISULFID 87 130
 FT DISULFID 77 77
 FT DISULFID 86 86
 FT CARBOHYD 33 33
 FT CARBOHYD 101 101
 SEQUENCE 149 AA: 17094 MW: 198EB3B8C745FEED CRC64;

Query Match 25.2%; Score 101.5; DB 1; Length 149;
 Best Local Similarity 32.2%; Pred. No. 8.1e-12;
 Matches 39; Conservative 21; Mismatches 60; Indels 1; Gaps 1;

QY 7 RLLLAALLQALPAQAPVSPDAPGHRKRVSMIDYTRATCPREVVVLYTEIMCTYAK 66
 DB 12 QLLTGLVLPVPTQWALSNGNISSEVEVVPFOQWMSRYSRVERVLIVSEYPSPEMH 71
 QY 67 QLVPSCVTVORGGCCPDGEGCVPTGQGVNMOILMR-YPSOQLGSELSHSCCECR 125
 DB 72 LSPSPSVSLMRCTGCCSDSMHCVPLETANVTMQLMKRYSLDOPFEVENSFSOHVACECK 131
 QY 126 P 126
 DB 132 P 132

RESULT 17

ID PLGF_HUMAN STANDARD: PRT: 221 AA.

AC P49763; Q9BV78; Q9Y6S8; Q07101;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Placenta growth factor precursor (PLGF).
 GN PGF OR PLGF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-1).
 RC TISSUE=placenta;
 RX MEDLINE=92021031; PubMed=1924389;
 RA Maglione D., Guerriero V., Vigiiletto G., Delli-Bovi P., Persico M.G.;
 RT "Isolation of a human placenta cDNA coding for a protein related to
 RT the vascular permeability factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9267-9271(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-2).
 RC TISSUE=placenta;
 RX MEDLINE=94198032; PubMed=8148155;
 RA Hauser S.D., Welch H.A.;
 RT "A heparin-binding form of placenta growth factor (PLGF-2) is
 RT expressed in human umbilical vein endothelial cells and in
 RT placenta.";
 RL Growth Factors 9:259-268(1993).
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM PLGF-2).
 RX MEDLINE=93205407; PubMed=7681160;
 RA Maglione D., Guerriero V., Vigiiletto G., Ferraro M.G., Aprelikova O.,
 RA Alfaiolo K., del Vecchio S., Lei K.-J., Chou J.Y., Persico M.G.;
 RT "Two alternative mRNAs coding for the angiogenic factor, placenta
 RT growth factor (PLGF), are transcribed from a single gene of
 RT chromosome 14.";
 RL Oncogene 8:925-931(1993).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-3).
 RC TISSUE=placenta;
 RX MEDLINE=97350807; PubMed=9207183;
 RA Cao Y., Ji W.-R., Qi P., Rosin A., Cao Y.;
 RT "Placenta growth factor: identification and characterization of a
 RT novel isoform generated by RNA alternative splicing.";
 RL Biochem. Biophys. Res. Commun. 235:493-498(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-1).
 RA Rowen L., Madan A., Qin S., Abbas N., Dors M., Dickhoff R., James R.,
 RA Loretz C., Lasky S., Madan A., Prescott S., Ratcliffe A., Shaffer T.,
 RA Hood L.;
 RT "Sequencing of human chromosome 14.";
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM PLGF-2).
 RC TISSUE=muscle, and placenta;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP CHARACTERIZATION, AND SEQUENCE OF 19-24.
 RX MEDLINE=95014370; PubMed=7929268;
 RA Park J.E., Chen H.H., Winer J., Houck K.A., Ferrara N.;
 RT "Placenta growth factor. Potential of vascular endothelial growth
 RT factor bioactivity, in vitro and in vivo, and high affinity binding
 RT to Flt-1 but not to Flt-1/KDR.";
 RL J. Biol. Chem. 269:25646-25654(1994).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) (ISOFORM PLGF-1).
 RX MEDLINE=21192270; PubMed=11069911;
 RA Iyer S., Leonidas D.D., Swaminathan G.J., Maglione D., Battisti M.,
 RA Tucci M., Persico M.G., Acharya K.R.;
 RT "The crystal structure of human placenta growth factor-1 (PLGF-1), an

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Rt angiogenic protein, at 2.0 Å resolution."
Rt J. Biol. Chem. 276:12153-12161(2001).
CC -1- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC cell growth, stimulating their proliferation and migration. It
CC binds to receptor VEGFR-1/Flt1. PlGF-2 binds neuropilin-1 and 2 in
CC a heparin-dependent manner.
CC -1- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
CC heterodimer with VEGF/VEGF-A. PlGF-3 is found both as homodimer
CC and as monomer.
CC -1- SUBCELLULAR LOCATION: The three forms are secreted but PlGF-2
CC appears to remain cell attached unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms: PlGF-1/PlGF-131, PlGF-2/PlGF-152
CC and PlGF-3 (shown here); are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: While the three forms are present in most
CC placental tissues, the PlGF-2 is specific to early (8 week)
CC placenta and only PlGF-1 is found in the colon and mammary
CC carcinomas.
CC -1- DOMAIN: PlGF-2 contains a basic insert which acts as a cell
CC retention signal.
CC -1- PTM: N-Glycosylated.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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-----
DR EMBL: X54936; CAA3698.1; -.
DR EMBL: S72960; AAB30462.2; -.
DR EMBL: S57152; AAB25832.2; ALT. SEQ.
DR EMBL: AC006530; AAD30179.1; -.
DR EMBL: BC001422; AAH01422.1; -.
DR EMBL: BC007789; AAH07789.1; -.
DR EMBL: BC007255; AAH07255.1; -.
DR EMBL: AB4411; CAA01393.1; -.
DR PDB: 1FZY; 09-MAY-01.
DR MIM: 601121; -.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR ProDom: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Heparin-binding;
KW Alternative splicing; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 221
FT DOMAIN 193 213 PLACENTA GROWTH FACTOR.
FT DISULFID 52 94 HEPARIN-BINDING (PROBABLE).
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 77 INTERCHAIN.
FT DISULFID 86 86 INTERCHAIN.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARPSPIC 132 203 MISSING (IN ISOFORM PlGF-1 AND ISOFORM
FT VARPSPIC 213 213 PLGF-2)
FT VARPSPIC 213 213 R -> RRRPKRGKRRRKQRPPTDCHL (IN ISOFORM
FT CONFLICT 91 91 PlGF-2).
FT SEQUENCE 221 AA; 24788 MW; D364C6A73C1C6987 CRC64;
Query Match 24.5%; Score 176.5; DB 1; Length 221;
Best Local Similarity 34.1%; Pred. No. 3.9e-11;
Matches 43; Conservative 18; Mismatches 60; Indels 5; Gaps 2;
3 PLRLRLLAALLQLAPAPVSPQPARPHGRKRVYSMDIYTRATQCPRRVYVPLVYELMG 62
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8 PFTDLLGLALPAVPPOOMALISAGNSSEVEYVFEQWGSSTYRALERLADVSEKPS 67

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OY      63  TVANKLVSCVYVQGGCCCPDDGLECVPTGHOVQRMILMR---YSSQSGESLSEH 119
          |||||: ||||| G: ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      68  EWEHMFSSCSVLKTCGCCGDENLHCVPETANTYMTOLKIRSGDS--YVELTFSDH 125
OY      120 SQCECR 125
          :|||
DB      126 VRCECR 131

RESULT 18
PGLF_RAT
ID      ID      PGLF_RAT      STANDARD:      PRT;      158 AA.
AC      063434:
DT      01-MAR-2002 (Rel. 41, Created)
DT      01-MAR-2002 (Rel. 41, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Placenta growth factor precursor (Pigf).
GN      PLGF.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_Taxid=10116;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX      MEDLINE=95221439; PubMed=7706320;
RA      Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,
RA      Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;
RT      "Purification and characterization of a naturally occurring vascular
RT      endothelial growth factor, placenta growth factor heterodimer.";
RL      J. Biol. Chem. 270:7717-7723(1995).
CC      -1- FUNCTION: Growth factor active in angiogenesis, and endothelial
CC      cell growth, stimulating their proliferation and migration. It
CC      binds to receptor VEGFR-1/Flt1 (By similarity).
CC      -1- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as
CC      heterodimer with VEGF/VEGF-A.
CC      -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL: LA0030; AAA97426.1; -.
DR      HSSP: P15692; IYBP.
DR      InterPro: IPR000072; PDGF.
DR      Pfam: PF00341; PDGF; 1.
DR      ProDom: PD001629; PDGF; 1.
DR      SMART: SM00141; PDGF; 1.
DR      PROSITE: PS00249; PDGF_1; 1.
DR      PROSITE: PS00278; PDGF_2; 1.
KW      Mitogen; Growth factor; Glycoprotein; Signal.
FT      SIGNAL 1 23
FT      CHAIN 1 158
FT      DISULFID 48 90 PLACENTA GROWTH FACTOR.
FT      DISULFID 79 125 INTRACHAIN (BY SIMILARITY).
FT      DISULFID 83 127 INTRACHAIN (BY SIMILARITY).
FT      DISULFID 73 73 INTRACHAIN (BY SIMILARITY).
FT      DISULFID 82 82 INTRACHAIN (BY SIMILARITY).
FT      CARBOHD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHD 30 30 N-LINKED (GLCNAC. . .).
FT      CAROHD 97 97 N-LINKED (GLCNAC. . .).
FT      CAROHD 97 97 N-LINKED (GLCNAC. . .).
SQ      SEQUENCE 158 AA; 17681 MW; B4771373A82E15B9 CRC64;

Query Match 24.5%; Score 176; DB 1; Length 158;
Best Local Similarity 36.2%; Pred. No. 3.2e-11;
Matches 47; Conservative 20; Mismatches 55; Indels 8; Gaps 4;

```


[illegible]

RESULT	21			
VEGF_RAT				
ID	VEGD_RAT	STANDARD:	PRT:	326 AA.
AC	035251;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (Figc).			
GN	FIGF OR VEGFD.			
OC	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RA	Yamada Y., Hirata Y., Nezu J., Shimane M.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1 FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flk4) receptor (By similarity).			
CC	-1 SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).			
CC	-1 SUBCELLULAR LOCATION: Secreted (By similarity).			
CC	-1 PM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).			
CC	-1 SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC	-----			
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CC	-----			
DR	EMBL; AF014827; AAB6557.1; -			
DR	HSSP; P15692; 1VP.			
DR	InterPro; IPR000072; PDGF.			
DR	Pfam; PF00341; PDGF_1.			
DR	ProDom; PD001629; PDGF; 1.			
DR	SMART; SM00141; PDGF_1.			
DR	PROSITE; PS00249; PDGF_1; 1.			
DR	PROSITE; PS50278; PDGF_2; 1.			
KW	Mitogen: Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.			
FT	SIGNAL	1	21	POTENTIAL.
FT	PROPEP	22	93	POTENTIAL.
FT	CHAIN	94	210	VASCULAR ENDOTHELIAL GROWTH FACTOR D.
FT	PROPEP	211	326	POTENTIAL.
FT	DOMAIN	227	317	4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
FT				1 (APPROXIMATE).
FT	REPEAT	227	242	2.
FT	REPEAT	263	278	3.
FT	REPEAT	282	298	4. (INCOMPLETE).
FT	REPEAT	306	317	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	116	158	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	147	194	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	151	196	INTRACHAIN (BY SIMILARITY).
FT	DISULFID	141	141	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	150	150	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	160	160	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	190	190	N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 37112 MM; 1261AFA373596C00 CRC64;
 Query Match 20.8%; Score 149.5; DB 1; Length 326;
 Best Local Similarity 32.3%; Pred. No. 3.5e-08;
 Matches 31; Conservative 16; Mismatches 44; Indels 5; Gaps 2;
 OY 34 KVSIVDIYTRATCOPREVYVPLVLELMGTAKQLVPSGVYQRCGCCDDGECPTG 93
 Db 105 KVID--EEMORQCSPRETCVAVASELKTNTTFKPCVAVNFRGCGCNESSVCMNTS 162
 OY 94 QHVRMOILMIRYPSQJGEM---SLEHSGCECRP 126
 Db 163 TSYSKOLFELISVPLTSVPELVPRVIAHNTGCKLP 198
 RESULT 22
 VEGC_MOUSE STANDARD; PRT; 415 AA.
 AC P97953;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-l).
 GN VEGFC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97164697; PubMed=9012504;
 RA STRAIN-BALB/C;
 RA Kukk E., Lymbousaki A., Taira S., Kaipainen A., Jeltsch M., Jounk V., Allitalo K.;
 RT "VEGF-C receptor binding and pattern of expression with VEGFR-3 suggests a role in lymphatic vascular development.";
 RL Development 122:3829-3837(1996).
 [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 108-126.
 RC STRAIN-BALB/C;
 RX MEDLINE=97388482; PubMed=9247316;
 RA Flitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R., Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciavarella A., Giannotti J., Finerly H., Zollner R., Beler D.R., Leak L.V., Turner K.J., Wood C.R.;
 RT "Characterization of murine Flt4 ligand/VEGF-C";
 RL Oncogene 15:613-618(1997).
 CC -1- FUNCTION: Growth factor active in angiogenesis, and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in angiogenesis of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
 CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expression detected in mesenchymal cells of postimplantation embryos, particularly in the regions where the lymphatic vessels undergo sprouting from embryonic veins, such as the perimetonephric, axillary and jugular regions, and in the developing mesenterium. Expressed in adult heart, brain, spleen, lung, liver, skeletal muscle and kidney.
 CC -1- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3, but only the fully processed form could activate VEGFR-2.
 CC VEGF-C first form an antiparallel homodimer linked by disulfide bonds. Before secretion, a cleavage occurs between arg-227 and ser-228 producing an heterotetramer. The next extracellular step of the processing removes the N-terminal propeptide. Finally the

CC mature VEGF-C is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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 CC -----
 CC EMBL: U73620; AAC52984.1; -;
 CC EMBL: U58112; AAB46707.1; -;
 CC HSSP: P15692; 1VPF.
 CC MGD: MGI:109124; VEGF.
 CC InterPro: IPR004153; CXXC.
 CC InterPro: IPR002400; GF_cysknob.
 CC InterPro: IPR000072; PDGF.
 CC Pfam: PF03128; CXXC; 5.
 CC Pfam: PF00341; PDGF; 1.
 CC PRINTS: PR00438; GRCYSKNOR.
 CC PRODOM: PD001629; PDGF; 1.
 CC SMART: SM00141; PDGF; 1.
 CC PROSITE: PS00249; PDGF_1; 1.
 CC PROSITE: PS0278; PDGF_2; 1.
 CC MitoGen: Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
 KW SIGNAL 31
 FT PROPEP 1 107
 FT CHAIN 108 223
 FT PROPEP 224 415
 FT DOMAIN 276 358
 FT REPEAT 276 291
 FT REPEAT 300 315
 FT REPEAT 324 339
 FT REPEAT 343 358
 FT DISULFID 127 169
 FT DISULFID 158 205
 FT DISULFID 162 207
 FT DISULFID 152 152
 FT DISULFID 161 161
 FT CARBOHYD 171 171
 FT CARBOHYD 201 201
 FT CARBOHYD 236 236
 SQ SEQUENCE 415 AA; 46471 MM; D9D3DD3CECC659D6 CRC64;
 Query Match 20.4%; Score 147; DB 1; Length 415;
 Best Local Similarity 32.7%; Pred. No. 8e-08;
 Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;
 OY 28 APGHQKVSIVDIYTRATCOPREVYVPLVLELMGTAKQLVPSGVYQRCGCCDDG 86
 Db 107 AAHNTETLKSIDEMKRTQCPREVCIDVKEGAATNTFFKPCVAVNFRGCGCNSSEG 166
 OY 87 LECVPTGQHVRMOILMIRYPSQJGEM---MSLEHSGCECRP 127
 Db 167 LQCMNTSTGYLSKTLFETVPLSGRPKPVITSFANHNSRCMSK 210
 RESULT 23
 VEGD_HUMAN STANDARD; PRT; 354 AA.
 AC O43915;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FlGF).
 GN FlGF OR VEGFD.
 OS Homo sapiens (Human).

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CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/cc	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; S67522; AAB29223.1; -.	
DR	HSSP; P15692; 2VPF.	
DR	InterPro; IPR000072; PDGF.	
DR	Pfam; PF00341; PDGF_1.	
DR	PRODOM; PD001629; PDGF; 1.	
DR	SMART; SM00141; PDGF_1.	
DR	PROSITE; PS00249; PDGF_1; FALSE.NEG.	
DR	PROSITE; PS50278; PDGF_2; 1.	
KW	Mitogen; Growth factor; Glycoprotein; Signal.	
FT	SIGNAL	1
FT		25
FT	CHAIN	26
FT		148
FT		
FT	DISULFID	46
FT		88
FT	DISULFID	77
FT		130
FT	DISULFID	81
FT		132
FT	DISULFID	71
FT		71
FT	DISULFID	80
FT		80
FT	CARBOHYD	95
FT		95
SO	SEQUENCE	148 AA; 16078 MW; FEI13BA104CC3F8 CRC64; N-LINKED (GLCNAC...)(POTENTIAL).

Query Match	20.28;	Score 145.5;	DB 1,	Length 148;
Best Local	Similarly	30.58,	Pred. No. 4e-08;	
Matches	39;	Conservative	23;	Mismatches 53;
				Indels 13;
				Gaps 4

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QY 7 RLLAALALQLPAPAPASOP--DAGHQRKRVSTIDVYTRATGCREVVEVPELVEMLTVA 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 QVVALLICMNLPECVSQSNDSPPTN--DWMRTLDKSGCKRDRIVYVLGEEYPESTN 64

QY 66 KQVPCSTYVRCGGCCGCPDQSLC--VPTGQHVQRMLIMIRP-----SGLGMSL 116
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 LQVMPCTYVRCGCGCGMDQQLCTAVETIRNTYTVASVGVSSSGTNGSGVSTNLRISY 124

QY 117 EHSQCEC 124
    : : : : :
Db 125 TEHTKDC 132

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RESULT	25
VEGC_HUMAN	
ID	VEGC_HUMAN
STANDARD:	PRT; 419 AA.
AC	P49767;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	vascular endothelial growth factor C precursor (VEGF-C) (Vascular endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-l).
GN	VEGFC.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID:9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX	MEDLINE=96178224; PubMed=8617204;
RA	Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kuk E.,
RA	Saksela O., Kalkkunen N., Alltalo K.;
RT	"A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RL	the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.",
EMBO J.	15:290-298(1996).
RN	[2]
RP	ERRATUM.
RX	MEDLINE=96203094; PubMed=8612600;
RA	Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kuk E.,
RA	Saksela O., Kalkkunen N., Alltalo K.;
EMBO J.	15:1751-1751(1996).
RN	[3]

RP SEQUENCE FROM N.A.
RC TISSUE-Glial tumor;
RX MEDLINE=96312526; PubMed=8700872;
RA Lee J., Gray A., Yuan J., Luo S.-M., Avraham H., Wood W.I.,
RT "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:11988-1992(1996).
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=97388482; PubMed=9247316;
RA Flitz L.J., Morris J.C., Towler P., Long A., Burgess J., Greco R.,
RA Wang Y., Gassaway R., Nickbarg E., Kovacic S., Ciardetta A.,
RA Giannotti J., Flinerty H., Zollner R., Beier D.R., Leak L.V.,
RA Turner K.J., Wood C.R.,
RT "Characterization of murine Flt4 ligand/VEGF-C.";
RL Oncogene 15:613-618(1997).
[5]
RN SEQUENCE OF 32-41; 112-121 AND 228-233, AND MUTAGENESIS OF ARG-227.
RX MEDLINE=97377029; PubMed=9233800;
RA Joukov V., Sorsa T., Kumar V., Jeltsch M., Claesson-Welsh L., Cao Y.,
RA Sarsela O., Kalkkinen N., Allalio K.;
RT "Proteolytic processing regulates receptor specificity and activity of
RT VEGF-C.";
RL EMBL J. 16:3898-3911(1997).
CC -1- PUNCTATION: Growth factor active in angiogenesis, and endothelial
CC cell growth, stimulating their proliferation and migration and
CC also has effects on the permeability of blood vessels. May
CC function in angiogenesis of the venous and lymphatic vascular
CC systems during embryogenesis, and also in the maintenance of
CC differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Spleen, lymph node, thymus, appendix, bone
CC marrow, heart, placenta, ovary, skeletal muscle, prostate, testis,
CC colon and small intestine and fetal liver, lung and kidney, but
CC not in peripheral blood lymphocyte.
CC -1- PM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3, but only the fully processed form could activate VEGFR-2.
CC VEGF-C first form an antiparallel homodimer linked by disulfide
CC bonds. Before secretion, a cleavage occurs between arg-227 and
CC ser-228 producing an heterotetramer. The next extracellular step
CC of the processing removes the N-terminal propeptide. Finally the
CC mature VEGF-C is composed mostly of two VEGF homology domains
CC (VHDS) bound by non-covalent interactions.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X94216; CAA63907.1; -;
DR EMBL; U43142; AAA85214.1; -;
DR EMBL; U58111; AAB02909.1; -;
DR HSSP; P15692; IVPF.
DR MIM; 601528; -;
DR InterPro; IPR004153; CXKCX.
DR InterPro; IPR002400; GF_cyskn0t.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF03128; CXKCX; 5.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GF_CYSKN0T.
DR PRODOM; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.

DR EMBL: X94216: CAA63907.1; -.
DR EMBL: U48142: AAA85314.1; -.
DR EMBL: U58111: AAB02909.1; -.
DR HSSP: P15692: IVPF.
DR MIM: 601528; -.
DR InterPro: IPR004153; CXKC.
DR InterPro: IPR002400; GE_cysknob.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF03128: CXKC; 5.
DR Pfam: PF00341; PDGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleaveage on pair of basic residues; Multigene family.


```

FT SIGNAL 1 31
FT PROPEP 32 111
FT CHAIN 112 227
FT PROPEP 228 419
FT DOMAIN 280 362
FT REPEAT 280 295
FT REPEAT 304 319
FT REPEAT 328 343
FT REPEAT 347 362
FT DISULFID 131 173
FT DISULFID 162 209
FT DISULFID 166 211
FT DISULFID 156 156
FT DISULFID 165 165
FT CARBOHYD 175 175
FT CARBOHYD 205 205
FT CARBOHYD 240 240
FT MUTAGEN 227 227
SO SEQUENCE 419 AA; 46883 MM; 9F598719DB3E014F CRC64;

Query Match
Best Local Similarity 32.7%; Score 145; DB 1; Length 419;
Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

OY 28 APCGKRVKVSIDVYTRAT-CQPREVVVPLTVELMGTVAKQVPSCVTVORCGCCPDG 86
DB 111 AAHYNEILKISINEMKTKOCMPREVCIDVGEFGVATNTFFKPCSVYRCGCGCNSG 170
OY 87 LECPTGQHVQRMQILMIRPSSQLGE---MSLEHSQCCRPK 127
DB 171 LQCMNTSTYLSKTLFTVPLSGPKPVTISFANHSCRCMSK 214

RESULT 26
PDGA_HUMAN STANDARD; PRT; 211 AA.
AC P04085;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
DE (PDGF-1).
GN PDGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88144463; PubMed=3422746;
RA Bonthron D.T., Morton C.C., Orkin S.H., Collins T.;
RT "Platelet-derived growth factor A chain: gene structure, chromosomal
RT location, and basis for alternative mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1492-1496(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=88174698; PubMed=2832727;
RA Rorsman F., Bywater M., Knott T.J., Scott J., Betsholtz C.;
RT "Structural characterization of the human platelet-derived growth
RT factor A-chain cDNA and gene: alternative exon usage predicts two
RT different precursor proteins.";
RL Mol. Cell. Biol. 8:571-577(1988).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=86203630; PubMed=3754619;
RA Betsholtz C., Johansson A., Heldin C.H., Westermark B., Lind P.,
RA Urdas M.S., Eddy R., Shors T.B., Philpott K., Mellor A.L., Knott T.J.,
RA Scott J.;
RT "cDNA sequence and chromosomal localization of human platelet-derived
RT growth factor A-chain and its expression in tumour cell lines.";

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RL Nature 320:695-699(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88030061; PubMed=3666150;
RA Hoppe J., Schumacher U., Eichner W., Welch H.A.;
RT "The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only
RT distantly related.";
RL FEBS Lett. 223:243-246(1987).
RN [5]
RP SEQUENCE OF 1-53 FROM N.A.
RX MEDLINE=93252628; PubMed=8486521;
RA Takimoto Y., Li W.Y., Wang Z.Y., Tong B.D., Deuel T.F.;
RT "Nucleotide sequence of the 5' region of the human platelet-derived
RT growth factor A-chain gene.";
RL Hiroshima J. Med. Sci. 42:47-52(1993).
RN [6]
RP ALTERNATIVE SPLICING.
RX MEDLINE=87287247; PubMed=3614363;
RA Tong B.D., Auer D.E., Jaye M., Kaplow J.M., Rices G., McConathy E.,
RA Drohan W., Deuel T.F.;
RT "cDNA clones reveal differences between human glial and endothelial
RT cell platelet-derived growth factor A-chains.";
RL Nature 328:619-621(1987).
RN [7]
RP ALTERNATIVE SPLICING.
RX MEDLINE=87287248; PubMed=3614364;
RA Collins T., Bonthron D.T., Orkin S.H.;
RT "Alternative RNA splicing affects function of encoded platelet-derived
RT growth factor A chain.";
RL Nature 328:621-624(1987).
RN [8]
RP INTERCHAIN DISULFIDE BONDS.
RX MEDLINE=92283833; PubMed=1317862;
RA Andersson M., Oestman A., Baeckstroem G., Hellman U.,
RA George-Nascimento C., Westermark B., Heldin C.-H.;
RT "Assignment of interchain disulfide bonds in platelet-derived growth
RT factor (PDGF) and evidence for agonist activity of monomeric PDGF.";
RL J. Biol. Chem. 267:11260-11266(1992).
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC short form; are produced by alternative splicing.
CC -1- DOMAIN: The long form contains a basic insert which acts as a cell
CC retention signal.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -1- DATABASE: NAME-R&D systems' cytokine mini-reviews: PDGF.
CC WWW="http://www.rndsystems.com/asp/g/sitebuilder.asp?bodyid=220".
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M21571; -; NOT_ANNOTATED_CDS.
DR EMBL; M03795; CAA27421.1; -.
DR EMBL; M06374; CAA29677.1; -.
DR EMBL; M20494; AAA60045.1; -.
DR EMBL; M20488; AAA60045.1; JOINED.
DR EMBL; M20489; AAA60045.1; JOINED.
DR EMBL; M20490; AAA60045.1; JOINED.
DR EMBL; M20491; AAA60045.1; JOINED.
DR EMBL; M20492; AAA60045.1; JOINED.

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DR EMBL: M20493; AAA60045.1; JOINED.
DR EMBL: M19988; AAA60046.1; -.
DR EMBL: M21571; AAA60046.1; JOINED.
DR EMBL: M19984; AAA60046.1; JOINED.
DR EMBL: M19985; AAA60046.1; JOINED.
DR EMBL: M19986; AAA60046.1; JOINED.
DR EMBL: M19987; AAA60046.1; JOINED.
DR EMBL: M19989; AAA60047.1; -.
DR EMBL: M21571; AAA60047.1; JOINED.
DR EMBL: M19984; AAA60047.1; JOINED.
DR EMBL: M19985; AAA60047.1; JOINED.
DR EMBL: M19986; AAA60047.1; JOINED.
DR EMBL: M19987; AAA60047.1; JOINED.
DR EMBL: A09204; CAA00830.1; -.
DR EMBL: S62078; AAB26566.1; -.
DR PIR: A28964; PFHUG1.
DR PIR: B28964; B28964.
DR HSSP: P01127; 1PDG.
DR MIM: J73430; -.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCSKN0T.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 86
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 123 123
FT DISULFID 132 132
FT CARBOHYD 134 134
FT VARSPPLIC 194 196
FT VARSPPLIC 197 211
FT CONFLICT 64 66
SQ SEQUENCE 211 AA; 24043 MW; 48633DE558EFA43 CRC64;

Query Match 17.9%; Score 129; DB 1; Length 211;
Best Local Similarity 28.8%; Pred. No. 2.9e-06;
Matches 34; Conservative 21; Mismatches 35; Indels 28; Gaps 6;

QY 45 ATCCPREVV-VPLVETLNGTVAKOLV-PCYTVORCGGCCPDGLEGCVPTGQHVRMOI 101
DB 94 AVCKRTVYIEIPRS-QVDPSTANFLIMPCVEVKRCCTCCMTSSVKQCPSRVHNRHVAV 152

QY 102 LMIRY-----PSSQLGMSLEHSSQEC-----RP-----KKKDSAVKP 135
DB 153 AKVEYVKKRKLKEVQRLEHLEHCACATTSINPDYREEDTGRPRESGKKRRKKRLKP 210

RESULT 27
PDGA_RABIT STANDARD: PRT; 213 AA.
AC P34007;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
DE (PDGF-1).
GN PDGFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=92246970; PubMed=1575749;
RA Nakahara K.-I., Nishimura H., Kuro-O M., Takewaki S.-I., Iwase M.,
RA Ohkubo A., Yazaki Y., Nagai R.;
RT "Identification of three types of PDGF-A chain gene transcripts in
RT rabbit vascular smooth muscle and their regulated expression during
RT development and by angiotensin II.";
RL Blochem. Biophys. Res. Commun. 184:811-818(1992).
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A1, A2 (SHOWN HERE) AND A3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- INDUCTION: THE FORM A3 IS SELECTIVELY INDUCED BY ANGIOTENSIN II.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VBGF FAMILY OF GROWTH FACTORS.
DR PIR: J50735; J50735.
DR PIR: PS0387; PS0387.
DR PIR: JN0248; JN0248.
DR HSSP: P01127; 1PDG.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR PRINTS: PR00438; GFCSKN0T.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
DR Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 89
FT CHAIN 90 213
FT SITE 158 162
FT DISULFID 131 179
FT DISULFID 135 181
FT DISULFID 125 125
FT DISULFID 134 134
FT CARBOHYD 136 136
FT VARSPPLIC 196 198
FT VARSPPLIC 197 213
SQ SEQUENCE 213 AA; 24005 MW; 28A9B7E50487F4C5 CRC64;

Query Match 17.7%; Score 127.5; DB 1; Length 213;
Best Local Similarity 30.1%; Pred. No. 4.1e-06;
Matches 34; Conservative 24; Mismatches 46; Indels 9; Gaps 5;

QY 19 AOAIVSOPAPRGHOKRVSMIDVTRATGQPREVV-VPLVETLNGTVAKOLV-PCYTV 75
DB 71 ARHVAEKRPAPVPVRRKRT-IEAIPALCKRTVYIEIPRS-QVDPSTANFLIMPCVEV 128

QY 76 GRGCGCCPDGLEGCVPTGQHVRMOILMIRY-----PSSQLGMSLEHSSQEC 124
DB 129 KRCCTCCMTSSVKQCPSRVHNRHVAVAVVEYVKKRKLKEVQRLEHLEHCAC 181

RESULT 28
PDGA_RAT STANDARD: PRT; 204 AA.
AC P28576;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

```

DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
 DE (PDGF-1).
 GN PDGFA OR RPAL.
 OS Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP MEDLINE-93305723; PubMed=8318539;
 RX Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
 RA "Conservation in sequence and affinity of human and rodent PDGF
 RT ligands and receptors.";
 RL Biochim. Biophys. Acta 1173:294-302(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9319115; PubMed=8447423;
 RA Katayose D., Ohe M., Yamuchi K., Ogata M., Shirato K., Fujita H.,
 RA Shihahara S., Takishima T.;
 RT "Increased expression of PDGF A- and B-chain genes in rat lungs with
 RT hypoxic pulmonary hypertension.";
 RL Am. J. Physiol. 264:L100-L106(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RA Xia Y., Feng L., Tang W.W., Wilson C.B.;
 RT "Cloning and expression of rat platelet-derived growth factor
 RT A-chain";
 RL J. Am. Soc. Nephrol. 3:622-622(1992).
 RN [4]
 RP SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).
 RC STRAIN-FISCHER 344; Tissue=Smooth muscle;
 RX MEDLINE-93225589; PubMed=8469035;
 RA Szabo P., Weksler D., Whittington E., Weksler B.B.;
 RT "The age-dependent proliferation of rat aortic smooth muscle cells is
 RT independent of differential splicing of PDGF A-chain mRNA.";
 RL Mech. Ageing Dev. 67:79-89(1993).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 CC TRANSFORMATION PROCESSES.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: a long form (shown here) and a
 CC short form: are produced by alternative splicing.
 CC -1- DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER
 CC FORM PREDOMINATES IN YOUNG (1 DAY OLD) RATS WHILE THE LONGER FORM
 CC BECOMES MORE PREVALENT DURING AGING.
 CC -1- DOMAIN: The long form contains a basic insert which acts as a cell
 CC retention signal.
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 CC PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -----
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 CC -----
 CC EMBL: L06884; AAB59683.1; -
 DR EMBL: Z14120; CAAV8490.1; -
 DR EMBL: D10106; BAA0987.1; -
 DR EMBL: L06238; AAA41932.1; -
 DR EMBL: S57864; AAB26134.2; -
 DR HSSP: P01127; 1PDC.
 DR InterPro: IPR002400; GF_cysknoc.
 DR InterPro: IPR00072; PDGF.
 DR Pfam: PF00341; PDGF.1.
 DR PRINTS: PR00438; GFCSKNOC.

DR Prodom: PD001629; PDGF: 1.
 DR SMART: SM00141; PDGF: 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS0278; PDGF_2; 1.
 KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
 KW signal.
 FT SIGNAL 1 20
 FT PROPEP 21 85 BY SIMILARITY.
 FT CHAIN 86 204 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
 FT SITE 158 162 RECEPTOR BINDING SITE (POTENTIAL).
 FT DISULFID 96 140 BY SIMILARITY.
 FT DISULFID 129 177 BY SIMILARITY.
 FT DISULFID 133 179 BY SIMILARITY.
 FT DISULFID 123 123 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 132 132 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT VARSPLIC 194 196 GRR -> DVR (IN SHORT ISOFORM).
 FT VARSPLIC 197 204 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 85 111 KRISDAIPAVCKRTVYIERSQVD -> REVLKRPPO
 FT CONFLICT FARPGRSFTRYGART (IN REF. 2).
 FT CONFLICT I -> T (IN REF. 3).
 FT SEQUENCE 119 119
 SQ SEQUENCE 204 AA; 23307 MW; FA413F74E86F742C CRC64;
 Query Match 17.7%; Score 127; DB 1; Length 204;
 Best Local Similarity 31.3%; Pred No. 4.5e-06;
 Matches 31; Conservativity 20; Mismatches 36; Indels 12; Gaps 5;
 QY 45 ANCPREVV-VPLVELMGTVAKQLV-PCVTVORCGCCPDGLEGVPTGOHVRMOI 101
 DB 94 AACKRTVYIYIERS-QVDPSTANFLIMPPCVYEVKRCCTCNCSTSVKCPRVHRSVAV 152
 QY 102 LMRV----PSSDLGMSLEFHSQCRCRKKDSAYKP 136
 DB 153 AKVEYRKKRLKEVQVRLEHLEAC---ATSNLNP 187
 RESULT 29
 PGCA_MOUSE STANDARD; PRT; 211 AA.
 AC P20033;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Platelet-derived growth factor, A chain precursor (PDGF A-chain)
 GN PDGFA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
 RC STRAIN-BALB/C;
 RX MEDLINE-94031105; PubMed=1340209;
 RA Roisman F., Betscholtz C.;
 RT "Characterization of the mouse PDGF A-chain gene. Evolutionary
 RT conservation of gene structure, nucleotide sequence and alternative
 RT splicing.";
 RL Growth Factors 6:303-313(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RC STRAIN-F9;
 RX MEDLINE-90169294; PubMed=2155144;
 RA Mercola M., Wang C., Kelly J., Brownlee C., Jackson-Grusby L.,
 RA Stiles C., Bowen-Pope D.;
 RT "Selective expression of PDGF A and its receptor during early mouse
 RT embryogenesis.";
 RL Dev. Biol. 138:114-122(1990).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE

RESULT	32	
PDGB_HUMAN		
ID	PDGB_HUMAN	STANDARD;
		PRT; 241 AA

RN [9]

SEQUENCE OF 26-241 FROM N.A.

RA MEDLINE=86164981; PubMed=3456904;
 RA Welch H.A., Seibald W., Schairer H.U., Hoppe J.;
 RT "The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase
 RT mRNA which codes for the sequence of the PDGF-B chain.";
 RL FERS Lett. 196;344-348(1986).
 RN [10]
 RP SEQUENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=84236121; PubMed=6329745;
 RA Johnson A., Heidln C.H., Wasteson A., Westermarck B., Deuel T.F.,
 RA Huang J.S., Seeburg P.H., Gray A., Ullrich A., Scrcce G.,
 RA Stroobant P., Waterfield M.D.;
 RT "The c-sis gene encodes a precursor of the B chain of
 RT platelet-derived growth factor.";
 RL Embo J. 3:921-928(1984).
 RN [11]
 RP SEQUENCE OF 82-110.
 RX MEDLINE=83197379; PubMed=6844921;
 RA Antoniadis H.N., Hunkapiller M.W.;
 RT "Human platelet-derived growth factor (PDGF): amino-terminal amino
 RT acid sequence.";
 RL Science 220:963-965(1983).
 RN [12]
 RP SEQUENCE OF 82-112.
 RX MEDLINE=83244981; PubMed=6306471;
 RA Waterfield M.D., Scrcce G.T., Whittle N., Stroobant P., Johnson A.,
 RA Wasteson A., Westermarck B., Heidln C.H., Huang J.S., Deuel T.F.;
 RT "Platelet-derived growth factor is structurally related to the
 RT putative transforming protein p28ts of simian sarcoma virus.";
 RL Nature 304:35-39(1983).
 RN [13]
 RP MUTAGENESIS, AND IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR
 RP BINDING.
 RX MEDLINE=92097530; PubMed=1661670;
 RA Clements J.M., Bowden L.J., Bloxidge R.E., Catlin G., Cook A.L.,
 RA Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R.,
 RA Hellewell P.G., Kiarvin P.M., Naye P.D., Richardson S.J., Brown D.,
 RA Chabwela S.B., Starry M., Winslow D.;
 RT "Two PDGF-B chain residues, arginine 27 and isoleucine 30, mediate
 RT receptor binding and activation.";
 RL Embo J. 10:4113-4120(1991).
 RN [14]
 RP INTERCHAIN DISULFIDE BONDS.
 RX MEDLINE=92283833; PubMed=1317862;
 RA Anderson M., Oestman A., Backstrom G., Hellman U.,
 RA George-Nascimento C., Westermarck B., Heidln C.H.;
 RT "Assignment of interchain disulfide bonds in platelet-derived growth
 RT factor (PDGF) and evidence for agonist activity of monomeric PDGF.";
 RL J. Biol. Chem. 267:11260-11266(1992).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=93010987; PubMed=1396586;
 RA Oefner C., D'Arcy A., Winkler F.K., Eggmann B., Hosang M.;
 RT "Crystal structure of human platelet-derived growth factor BB.";
 RL Embo J. 11:3921-3926(1992).
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC -1- SUBUNIT: ANTI-PARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 CC TRANSFORMATION PROCESSES.
 CC -1- PHARMACEUTICAL: Available under the name Reggrenex (Ortho-McNeil).
 CC used to promote healing in diabetic neuropathic foot ulcers.
 CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
 CC PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC -1- DATABASE: NAME-R&D Systems' cytokine source book: PDGF;
 CC WWW="http://www.rndsystems.com/asp/4/sitebuilder.asp?bodyid=220".
 CC -1- DATABASE: NAME-Reggrenex; NOTE=Clinical information on Reggrenex;
 CC WWW="http://www.reggrenex.com/".
 CC -----
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CC -----
DR EMBL; K01401; AAA60552.1; -.
DR EMBL; K01918; AAA60552.1; JOINED.
DR EMBL; J00121; AAA60552.1; JOINED.
DR EMBL; K01398; AAA60552.1; JOINED.
DR EMBL; K01399; AAA60552.1; JOINED.
DR EMBL; K01400; AAA60552.1; JOINED.
DR EMBL; X02811; CAA26579.1; -.
DR EMBL; M12783; AAA60553.1; -.
DR EMBL; X02744; CAA26524.1; -.
DR EMBL; K01917; AAA98793.1; -.
DR EMBL; K01913; AAA98793.1; JOINED.
DR EMBL; K01914; AAA98793.1; JOINED.
DR EMBL; K01915; AAA98793.1; JOINED.
DR EMBL; K01916; AAA98793.1; JOINED.
DR EMBL; X03702; CAA27333.1; -.
DR EMBL; Z81010; CAB20535.1; -.
DR EMBL; X00561; CAA25228.1; -.
DR EMBL; X00561; CAA25229.1; -.
DR EMBL; X98706; CAA67262.1; -.
DR PIR; A94276; PFHUG2.
DR PDB; 1PDG; 3I-JUN-94.
DR MM; 190040; -.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GF_CYSKNOT.
DR PRODOM; PD001629; PDGF_1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal;
KW Pharmaceutical; 3D-structure.
FT SIGNAL 1 20
FT CHAIN 21 81
FT CHAIN 82 190
FT PROPSEP 191 241
FT SITE 108 108
FT SITE 111 111
FT DISULFID 97 141
FT DISULFID 130 178
FT DISULFID 134 180
FT DISULFID 124 124
FT DISULFID 133 133
FT CONFLICT 21 21
FT CONFLICT 101 101
FT CONFLICT 105 105
PLATELET-DERIVED GROWTH FACTOR, B CHAIN.
INVOLVED IN RECEPTOR BINDING.
INTERCHAIN.
E -> R (IN REF. 3).
T -> E (IN REF. 11).
E -> C (IN REF. 11).
Query Match 17.1%; Score 123; DB 1; Length 241;
Best Local Similarity 34.8%; Pred. No. 1,4e-05;
Matches 31; Conservative 17; Mismatches 29; Indels 12; Gaps 4;
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OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TEXEL; TISSUE=Spleen;
RA Woodall C.J., Zhang Z., Walt N.J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
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CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X97123; CA65790.1; -
DR HSSP; P01127; 1PDG.
DR InterPro; IPR000240; GF_cysknott.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KM Mitogen; Growth factor; Proto-oncogene; Platelet; Signal.
FT SIGNAL 1 20
FT PROPEP 21 81
FT CHAIN 82 190
FT PROPEP 191 241
FT SITE 108 108
FT SITE 111 111
FT DISULFID 97 141
FT DISULFID 130 178
FT DISULFID 134 180
FT DISULFID 124 124
FT DISULFID 133 133
FT CARBOHYD 63 63
SQ SEQUENCE 241 AA; 27331 MW; 37BE1EC12E7D2863 CRC64;

Query Match 15.0%; Score 108; DB 1; Length 241;
Best Local Similarity 32.6%; Pred. No. 0.00047;
Matches 28; Conservative 14; Mismatches 38; Indels 6; Gaps 3;

OY 45 ATCPREVYVLYVLELMG-TYAKOLY-PSCTVYQRCGCCDDGEGCPTGQHYRMQTL 102
DB 95 AECKTREVESISRRLIDRTIANLWMPCEVQRCSCNNRNVCAPTOVDKRYOVK 154
OY 103 MIRPSS-----QLGEMSLDEHSOCEC 124
DB 155 KIEIVRKKKIRKATVTLVDHLACRC 180

RESULT 37
VEGC_RAT STANDARD: PRT: 126 AA.
AC 035757;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor C precursor (VEGF-C) (Vascular
```

```
DE endothelial growth factor related protein) (VRP) (Flt4 ligand) (Flt4-
DE L) (Fragment).
GN VEGFC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RA Mandirola S.J., Pepper M.S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth factor active in angiogenesis and endothelial
CC cell growth, stimulating their proliferation and migration and
CC also has effects on the permeability of blood vessels. May
CC function in angiogenesis of the venous and lymphatic vascular
CC systems during embryogenesis, and also in the maintenance of
CC differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3, but only the fully processed form could activate VEGFR-2.
CC VEGF-C first form an antiparallel homodimer linked by disulfide
CC bonds. Before secretion, a cleavage occurs between arg-227 and
CC ser-228 producing an heterotetramer. The next extracellular step
CC of the processing removes the N-terminal propeptide. Finally the
CC mature VEGF-C is composed mostly of two VEGF homology domains
CC (VHDS) bound by non-covalent interactions (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL; AF010302; AAB63248.1; -
DR HSSP; P15692; 2VPF.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR PRODOM; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS00249; PDGF_1; 1.
KM Mitogen; Growth factor; Glycoprotein;
KW Cleavage on pair of basic residues; Multigene family.
FT NON_TER 1 1
FT CHAIN 1 71
FT PROPEP 72 126
FT DISULFID 6 53
FT DISULFID 10 55
FT DISULFID 9 9
FT CARBOHYD 19 19
FT CARBOHYD 49 49
FT CARBOHYD 84 84
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13977 MW; 8F365AFBC4E037B0 CRC64;

Query Match 14.5%; Score 104.5; DB 1; Length 126;
Best Local Similarity 36.2%; Pred. No. 0.00056;
Matches 21; Conservative 9; Mismatches 25; Indels 3; Gaps 1;

OY 73 VTVORGGCCPDGECPTGQHYRMQTLIRYPSOLGE---MSLEHSGCECRPK 127
DB 1 VSVYRCGGCCNSEGLQCMNTSTGYLSKTLFETVPLSDGPKFVTTISFANHSCROMSK 58

RESULT 38
DNM2_MYCLE
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ID DNJ2.MYCLE STANDARD: PRT: 378 AA.
 AC 049762;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chapterone protein dnaj2.
 GN DNAD2 OR ML0625 OR B1937_F2_56.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacterium.
 OX NCBI_Taxid=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R., Rodison K.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus."
 RL Nature 409:1007-1011(2001).
 CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,
 THE ATPASE ACTIVITY OF DNK (BY SIMILARITY).
 CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE DNK FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.
 CC -----
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 CC -----
 DR EMBL: 000016; AAA17167.1; -;
 DR EMBL: AL583919; CAC30133.1; -;
 DR HSP: P25685; 1HDJ.
 DR LepToma; ML0625; -;
 DR InterPro: IPR003095; DnaJ.
 DR InterPro: IPR002939; DnaJ_C.
 DR InterPro: IPR001305; DnaJ_CXXCXXG.
 DR InterPro: IPR001623; DnaJ_N.
 DR Pfam: PF00226; DnaJ; 1.
 DR Pfam: PF01556; DnaJ_C; 1.
 DR Pfam: PF00684; DnaJ_CXXCXXG; 1.
 DR PRINTS: PR00625; DnaJPROTEIN.
 DR SMART: SM00271; DnaJ; 1.
 DR PROSITE: PS00636; DnaJ_1; FALSE_NEG.
 DR PROSITE: PS0076; DnaJ_2; 1.
 DR PROSITE: PS00637; DnaJ_CXXCXXG; FALSE_NEG.
 DR Chapterone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
 KW Complete proteome.
 FT DOMAIN 4 68 J-DOMAIN.
 FT DOMAIN 80 111 GLY-RICH.
 FT REPEAT 141 148 CXXCXXG MOTIF.
 FT REPEAT 158 165 CXXCXXG MOTIF.
 FT REPEAT 184 191 CXXCXXG MOTIF.
 FT REPEAT 198 205 CXXCXXG MOTIF.
 FT METAL 141 141 ZINC 1 (BY SIMILARITY).
 FT METAL 144 144 ZINC 1 (BY SIMILARITY).
 FT METAL 158 158 ZINC 2 (BY SIMILARITY).

FT METAL 161 161 ZINC 2 (BY SIMILARITY).
 FT METAL 184 184 ZINC 2 (BY SIMILARITY).
 FT METAL 187 187 ZINC 2 (BY SIMILARITY).
 FT METAL 198 198 ZINC 1 (BY SIMILARITY).
 FT METAL 201 201 ZINC 1 (BY SIMILARITY).
 SQ SEQUENCE 378 AA: 40399 MW: 723DD8BF6FC62153 CRC64;
 Query Match 10.8%; Score 78; DB 1: Length 378;
 Best Local Similarity 23.3%; Pred. No. 0.9;
 Matches 30; Conservative 18; Mismatches 49; Indels 32; Gaps 4;
 QY 29 PGHQRKVSMDVYTRATCPREVV-----PLTVLMLG-----T 63
 Db 110 PGSDSLPMWLDIECATYGTQVYDFAVLCDRCOGKGTNGSDAPICPTCGRGREYOT 169
 QY 64 VAROLVPCVTVQVRCGC-----CPDDGLECYPTGHOVROMIIMIRYPSQLGEMSL 117
 Db 170 VQSLGQWYVTRPCTPCRGVGVYIPDCCQCVGDGRVRRAREI-YKIPISGVGDGRVR 228
 QY 118 EHSQCECRP 126
 Db 229 LAAQGEVGP 237
 RESULT 39
 ID YN81.CAEEL STANDARD: PRT: 1416 AA.
 AC 003610;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 316.1 kDa protein ZC84.1 in chromosome III.
 GN ZC84.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodermata; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille F., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Spoat J.,
 RA Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN [2]
 RP REVISIONS.
 RC STRAIN-BRISTOL N2;
 RA Jones S.J.M.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO D104.3.
 CC -1- SIMILARITY: CONTAINS 5 BPT1/KUNITZ INHIBITOR DOMAINS.
 CC -----
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 CC -----
 DR EMBL: Z19157; CAA79569.1; -;

DR PIR: S28291; S28291.
DR HSSP: P00974; 1BRB.
DR WormPep: ZC84.1; CE15020.
DR InterPro: IPR002899; EB.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF01683; EB; 3.
DR Pfam: PF00014; Kunitz_BPTI; 5.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00131; KU; 5.
DR SMART: SM00289; WRL; 13.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 5.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
KW Hypothetical protein; Serine protease inhibitor; Repeat.
FT DOMAIN 212 266 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 337 387 BPTI/KUNITZ INHIBITOR 2.
FT DOMAIN 434 484 BPTI/KUNITZ INHIBITOR 3.
FT DOMAIN 538 590 BPTI/KUNITZ INHIBITOR 4.
FT DOMAIN 646 698 BPTI/KUNITZ INHIBITOR 5.
SQ SEQUENCE 1416 AA; 152986 MW; 531CACE1CB22E70D CRC64;

Query Match Best Local Similarity 10.2%; Score 73.5; DB 1; Length 1416;
Matches 40; Conservative 21; Mismatches 39; Indels 69; Gaps 12;

QY 18 PAQAPVSQDPAP-----GHQ-----RKVSWIDYVTRATCOPREVVPPLTVELMG 62
DB 1037 PEKCVQSNCPGRGFAOKSLAGHVCCTVRKV-----ACESNEVILE-----G 1080
QY 63 TVAKQIVP--SCVTVQRC--GCGCPDGLGCVPT-----GQHQVRA--QILM--IRY 106
DB 1081 ECHAQVPSGSECLANECTGGSVCEDAKCECRPLKAVGFGQGEIQCSSNQVLANGLCH 1140
QY 107 PSSOLGEMSL-----EHS-----QCECR-----PKKKDSAV 133
DB 1141 NKAATGEMCLTVRQCGENSGCIEGSCCKKFKFKACKMTPVEKKSAV 1189

RESULT 40
GRN_CAVPO STANDARD; PRT; 591 AA.
ID GRN_CAVPO
AC P28797;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulin 2;
DE Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
DE (Fragment).
GN GRN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
ON NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
RC TISSUE=Testis; PubMed=8471244;
RA Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Aral Y.,
RA Gerton G.L.;
RT "Acrogranin, an acrosomal cysteine-rich glycoprotein, is the
RT precursor of the growth-modulating peptides, granulins, and
RT epithelins, and is expressed in somatic as well as male germ cells."
RL Mol. Reprod. Dev. 34:233-243(1993).
CC -1- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
CC
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CC -----
DR EMBL: M86735; AAA37030.1; "
DR InterPro: IPR000118; Granulin.
DR Pfam: PF00396; granulin; 7.
DR SMART: SM00277; GRAN; 6.
DR PROSITE: PS00799; GRANULINS; 6.
KW Cytokine; Repeat; Signal; Glycoprotein.
FT NON_TER 1 3
FT SIGNAL <1 1
FT CHAIN 4 591 ACGROGRANIN.
FT PEPTIDE 753 798 GRANULIN 1.
FT PEPTIDE 711 764 GRANULIN 2.
FT PEPTIDE 206 261 GRANULIN 3.
FT PEPTIDE 281 335 GRANULIN 4.
FT PEPTIDE 737 745 GRANULIN 5.
FT PEPTIDE 439 494 GRANULIN 6.
FT PEPTIDE 751 769 GRANULIN 7.
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 591 AA; 62586 MW; E87C9FC8F21CB8A1 CRC64;

Query Match Best Local Similarity 10.1%; Score 72.5; DB 1; Length 591;
Matches 31; Conservative 17; Mismatches 51; Indels 41; Gaps 6;

QY 8 LLLAALLDLAFAO-----APVSQDPAGHQKRVSWIDYVTRATCOPREVVPPLT 57
DB 338 LLOYPMQKTRQAPSRSPGPRPPRPLRSISQDEV---VSCRGN----- 389
QY 58 VELMGTVAKQIVPSCVTVQRCGCGCP--DDGLECVPTGQHYVMQILMIRPS-----SQL 111
DB 390 -----CCRLASGEMGCCPSSEGLYCMAGERCQVGDRLAPKMAHMLSLST 436
QY 112 GEMSLSEHSQC-----ECRPK 127
DB 437 TDVGDQDHASCPVRQTCCKP 456

RESULT 41
CYAA_RAT STANDARD; PRT; 1064 AA.
ID CYAA_RAT
AC P26770;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Adenylate cyclase, type IV (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Adenyllyl cyclase).
GN ADCY4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis; PubMed=1946437;
RA Gao B., Gilman A.G.;
RA Medline=92052234;
RT "Cloning and expression of a widely distributed (type IV) adenylyl
RT cyclase."
RL Proc. Natl. Acad. Sci. U.S.A. 88:10178-10182(1991).
CC -1- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-INSENSITIVE ADENYLYL
CC CYCLASE.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -1- ENZYME REGULATION: INSENSIBLE TO CA(2+)/CALMODULIN. STIMULATED BY
CC THE G PROTEIN BETA & GAMMA SUBUNIT COMPLEX.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE

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CC      FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M80633; AAA0665.1; -.
DR      PIR: A41542; A41542.
DR      HSSP: P26769; IAB8.
DR      InterPro: IPR001054; Guanylyl_cyclase.
DR      Pfam: PF00211; guanylate_cyc; 2.
DR      SMART: SM00044; CYC; 2.
DR      PROSITE: PS00452; GUANYLATE_CYCLASES_1; 2.
DR      PROSITE: PS00125; GUANYLATE_CYCLASES_2; 2.
KW      Lyase; CAMP synthetis; Transmembrane; Glycoprotein; Duplication.
FT      DOMAIN 1 28
FT      TRANSMEM 29 50 POTENTIAL.
FT      TRANSMEM 61 80 POTENTIAL.
FT      TRANSMEM 94 117 POTENTIAL.
FT      TRANSMEM 120 138 POTENTIAL.
FT      TRANSMEM 141 162 POTENTIAL.
FT      TRANSMEM 170 190 POTENTIAL.
FT      DOMAIN 191 582 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 583 604 POTENTIAL.
FT      TRANSMEM 608 630 POTENTIAL.
FT      TRANSMEM 661 684 POTENTIAL.
FT      DOMAIN 685 707 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 708 733 POTENTIAL.
FT      TRANSMEM 741 761 POTENTIAL.
FT      TRANSMEM 788 804 POTENTIAL.
FT      DOMAIN 805 1064 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 694 694 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 1064 AA; 118798 MW; 5A2A0B895B5A0DA8 CRC64;

Query Match 10.1%; Score 72.5; DB 1; Length 1064;
Best Local Similarity 25.6%; Pred. No. 9.4;
Matches 31; Conservative 19; Mismatches 40; Indels 31; Gaps 8;

QY 4 LTRRLLLAALLQLAPAPVSPD-----APGHQKVVSMIDV--YTR--ATCQPR 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 235 LAEMAEIARQAQOS--SRPENTNNHSLVYKRHGVSYLADIYGTRLASECSPK 292
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 51 EYVVPPLTVELMG--TVAKQLVPSCVTVORCGGC-----CPDDGLECVPTGOHOV 97
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 293 ELVLMIN-ELFGKFDIAKE--HECMRIKILGDCYVCVSGPLPLDPHAINCVRMGLDMC 349
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 98 R 98
DB 350 R 350

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RX      MEDLINE-98256315; PubMed-9593731;
RA      Peng J. M., Marshall N.F., Price D.H.;
RT      Identification of a cyclin subunit required for the function of
RT      Drosophila P-TEFb.
RL      J. Biol. Chem. 273:13855-13860(1998).
CC      -1- FUNCTION: REGULATORY SUBUNIT OF THE CYCLIN-DEPENDENT KINASE PAIR
CC      (CDK9/CYCLIN T) COMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION
CC      ELONGATION FACTOR B (P-TEFb), WHICH IS PROPOSED TO FACILITATE THE
CC      TRANSCRIPTION FROM ABORTIVE TO PRODUCTION ELONGATION BY
CC      PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE
CC      SUBUNIT OF RNA POLYMERASE II (RNAP II).
CC      -1- SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFb.
CC      -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF051933; AAC73052.1; -.
DR      FlyBase: FBgn0025455; Cyct.
DR      InterPro: IPR000553; Cyclin.
DR      Pfam: PF00134; cyclin; 1.
DR      SMART: SM00385; CYCLIN; 2.
KW      Cyclin; Transcription regulation.
FT      DOMAIN 15 21
FT      TRANSMEM 382 390 POLY-SER.
FT      DOMAIN 426 429 POLY-SER.
FT      DOMAIN 441 449 POLY-SER.
FT      DOMAIN 553 556 POLY-SER.
FT      DOMAIN 598 603 POLY-PRO.
FT      DOMAIN 872 880 POLY-LYS.
FT      DOMAIN 993 998 POLY-GLY.
SQ      SEQUENCE 1097 AA; 118401 MW; AD55F3F57BCD3D6B CRC64;

Query Match 10.1%; Score 72.5; DB 1; Length 1097;
Best Local Similarity 24.6%; Pred. No. 9.7;
Matches 32; Conservative 19; Mismatches 36; Indels 43; Gaps 6;

QY 4 LTRRLLLAALLQLAPAPVSPD-----PQHQRKVVSMIDVYTRATCOPREVVVPTVEL 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 788 LVRSLLKES---LCPNNAISLTKDALTMGLK-----PADELLEPR----- 825
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 MGTVAQLVPSCVTVORCGGCCPDGIECVPTGOHOVQMQLIMIRYSSQLGEMSLSEHS 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 826 -----PAPATIRKEGDTPTMTSLASGPAP-----MDLEVPTRQAGEIKESSES 868
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 QCECRPKKKD 130
DB 869 KSE-KKKKKD 877

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RESULT 42
CCT_DROME
ID CCT_DROME STANDARD: PRT; 1097 AA.
AC 096433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin T.
GN CYCT.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RX [1]
RP SEQUENCE FROM N.A.
RA Acampora D., D'Esposito M., Falella A., Pannese M., Migliaccio E.,

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```

RESULT 43
HXB2_HUMAN
ID HXB2_HUMAN STANDARD: PRT; 356 AA.
AC P14652; P17485; P10913;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Homeobox protein Hox-B2 (Hox-2h) (Hox-2.8) (K8).
GN HOXB2 OR HOX2H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-90098876; PubMed-2574852;
RA Acampora D., D'Esposito M., Falella A., Pannese M., Migliaccio E.,

```

RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
 RT "The human HOX gene family";
 RL Nucleic Acids Res. 17:10385-10402(1989).
 RN [2]
 RP SEQUENCE OF 132-208 FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-89378558; PubMed-2570724;
 RA Giampao A., Acampora D., Zappavigna V., Pannese M.,
 RA D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G.,
 RA Simeone A., Boncinelli E., Peschle C.;
 RT Differential expression of human HOX-2 genes along the anterior-
 RL posterior axis in embryonic central nervous system";
 [3]
 RN SEQUENCE OF 143-208 FROM N.A.
 RX MEDLINE-90215256; PubMed-2576652;
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
 RT "Organization of human class I homeobox genes";
 RL Genome 31:745-756(1989).
 [4]
 RN SEQUENCE OF 143-202 FROM N.A.
 RX MEDLINE-88329001; PubMed-2901346;
 RA Kongsuwan K., Webb E., Housiaux P., Adams J.M.;
 RT "Expression of multiple homeobox genes within diverse mammalian
 RL haemopoietic lineages";
 RN EMBO J. 7:2131-2138(1988).
 [5]
 RP SEQUENCE OF 1-42 FROM N.A.
 RX MEDLINE-95181447; PubMed-7876223;
 RA Vialle-Grojean I., Huber P.;
 RT "Transcription factor GATA-1 regulates human HOXB2 gene expression in
 RL erythroid cells";
 RL J. Biol. Chem. 270:4544-4550(1995).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT
 CC 5-9 WEEKS FROM CONCEPTION.
 CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
 CC PROSCIPEDIA SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X16665; CAA34655.1; -
 DR EMBL: X16176; CAA34298.1; -
 DR EMBL: X14571; CAA32709.1; -
 DR EMBL: X78978; CAA55581.1; -
 DR PIR: S07542; MTHUZH.
 DR PIR: E37042; E37042.
 DR HSSP: P14653; 1B72.
 DR TRANSFAC: T03323; -
 DR MIM: 142967; -
 DR InterPro: IPR001827; Antennapedia.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00025; ANTENNAPEDIA.
 DR SMART: SM00024; HOMEBOX.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00032; ANTENNAPEDIA; 1.
 DR PROSITE: PS0071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW transcription regulation.
 FT DOMAIN 94 99 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 143 202 HOMEBOX.

FT CONFLICT 136 138 PEA -> RRL (IN REF. 2).
 SQ SEQUENCE 356 AA; 37913 MW; D7ACA0E3D5EBFB9 CRC64;
 Query Match 10.0%; Score 72; DB 1; Length 356;
 Best Local Similarity 31.8%; Pred. No. 3.5;
 Matches 27; Conservative 7; Mismatches 33; Indels 18; Gaps 5;
 QY 18 PAQAPVSPQAPAGHQKRVVSMIDVYTRATQPRVVV-----PLTVELMGTVAKQLV 69
 DB 224 PAERPAPSPGPPASR--AAM-----EACCHPEPVGALSADRPPLAVRLGAGASS-- 274
 QY 70 PSCVTVORCGGCCPDDELCVPTGO 94
 DB 275 PGC-ALRGAGLEPGLPEDFVFSGR 298
 RESULT 44
 ID SM3C_MOUSE STANDARD; PRT; 751 AA.
 AC 062181;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Semaphorin 3C precursor (Semaphorin E) (Sema E).
 GN SEMA3C OR SEMAE OR SEME.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NMRT: TISSUE-Embryo;
 RX MEDLINE-95267431; PubMed-7748561;
 RA Preschel A.W., Adams R.H., Betz H.;
 RT "Nurine semaphorin D/collapsin is a member of a diverse gene family
 RT and creates domains inhibitory for axonal extension.";
 RL Neuron 14:941-948(1995).
 CC -1- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
 CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. MAXIMUM
 CC EXPRESSION BETWEEN DAYS 10-12 WITH MODERATE LEVELS FROM DAY 13
 CC UNTIL BIRTH.
 CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X85994; CAA59986.1; -
 DR MGD: MGI:107557; Sema3c.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003659; PSI.
 DR InterPro: IPR001627; Sema.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF01403; Sema; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00423; PSI; 1.
 KW signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein;
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 751 SEMAPHORIN 3C.
 FT DOMAIN 237 535 SEMA.
 FT DOMAIN 636 716 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 714 717 POLY-GLN.

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FT DOMAIN 724 745 ARG/LYS-RICH (BASIC).
FT DISULFID 643 709 BY SIMILARITY.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 751 AA: 85259 MW: A9B5995E7DBA5D8 CRC64;

Query Match 9.9%; Score 71; DB 1; Length 751;
Best Local Similarity 23.5%; Pred. No. 9.5;
Matches 28; Conservative 16; Mismatches 37; Indels 38; Gaps 5;

OY 54 VPLTVELMTAKQLVPSC-----VTVORC---GGCCPD-----DGLCC---V 90
DB 484 VPTTWEISSKROQLYSSNEGVSQSLRCHITGTACDCCICARDPYCAMDGHSCSREFY 543
OY 91 PFGOHVRMQIIMIRYPSQSGEMSLSEHSQC-----ECRPKKDSAVK 134
DB 544 PFGKRSRQDYRHGNPLTQCRGFNKAIRNAEIVQYGRNNSTPLECAPSPQASIK 602

RESULT 45
YL00_MYCTU STANDARD; PRT: 550 AA.
AC 010709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 58.9 kDa protein RV2100 precursor.
GN RV2100 OR MT2160 OR MTCY49.40.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=968295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Peltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Ruter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Emolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV3776.
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CC -----
DR EMBL: Z73966; CAA98210.1; -.
DR EMBL: AE007065; AAK46441.1; ALT_INIT.
DR TIGR: MT2160; -.
DR Tuberculist; RV2100; -.
DR InterPro; IPR003870; DUF222.
DR InterPro; IPR002711; HNH.
DR InterPro; IPR003615; HNH_nuc.
DR Pfam; PF02720; DUF222; 1.
DR SMART; PF01844; HNH; 1.
DR SMART; SM00507; HNHc; 1.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 550 HYPOTHETICAL PROTEIN RV2100.
SQ SEQUENCE 550 AA: 58934 MW: B6BF18EC4188A7CE CRC64;

Query Match 9.8%; Score 70.5; DB 1; Length 550;
Best Local Similarity 26.2%; Pred. No. 7.8;
Matches 38; Conservative 17; Mismatches 49; Indels 41; Gaps 8;

OY 8 LLLAALLQAPAPQPSQDADGHRKVVSWIDY-----TRATCQREVYVPLTVEL 60
DB 167 LLDAALEHAGAWPLS---APRLEKAIQSWIDRDPGALRRSRISARTRDICIGDPDED 223
OY 61 MGTVA---KQLVPCVTYVOR-----CGCCPDGGLCEVPTGOHVRMQIIMIRYPSQSG 112
DB 224 AGTAAIMGRLYATDAMIDRLRLEMAHGYCEDD-----PRTLAQR-----ADALG 269
OY 113 EMSL-EHSSQCECRPKKDSAVKPD 136
DB 270 ALAAGADHILACGCG-----KPD 286
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Search completed: September 10, 2002, 02:57:35
Job time: 493 sec

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RESULT 2
Q91ZE1 PRELIMINARY: PRT: 190 AA.
AC Q91ZE1:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN VEGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Marlon S.; Lee T.-C.;
RT "Cloning of multiple VEGF splice variants from hypoxic neonatal rat
RT cardiomyocytes."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY033506; AL07526.1; -.
SQ SEQUENCE 190 AA; 22396 MW; 58937401041F377 CRC64;

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```

Query Match 37.5%; Score 269.5; DB 11; Length 190;
Best Local Similarity 43.8%; Pred. No. 4.6e-22;
Matches 57; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

```

```

QY 10 LALLQLAPAPVSPDAPGHR--KYVSWIDVYTRATCCPREVVVPLTVELMGTVAK 67
DB 12 LALLLYLHNAKSAQAPPTGEGKAEVKKFMDVYORSTCRPIETLVDFQETPEIETI 71
QY 68 LVPSCVTVORCGCCPRDGLCEVPTGOHVRMOILMIR-YPSOIGEMSLSEHSQCECRP 126
DB 72 FKPSCVPLMRGCGCCNDEALCEVPTSESNTTQIMRIKPHQSHIGEMSLFQHSRCECRP 131
QY 127 KKKDSAVKRPD 136
DB 132 KK--DRTKPE 139

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RESULT 3
Q9QX39 PRELIMINARY: PRT: 190 AA.
AC Q9QX39:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN VEGF.
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Spalacinae;
OC Spalax.
OX NCBI_TaxID=30637;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99313148; PubMed=10386577;
RA Avivi A., Resnick M.B., Nevo E., Joel A., Levy A.P.;
RT "Adaptive hypoxic tolerance in the subterranean mole rat Spalax
RT ehrenbergi: the role of vascular endothelial growth factor."
RL FBS Lett. 452:133-140(1999).
DR EMBL: AF186236; AAD56245.1; -.
DR HSSP: P15692; 2VPE.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR PRODOM: PD001629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22488 MW; 2228383BC65F0BFE CRC64;

```

```

Query Match 37.3%; Score 268.5; DB 11; Length 190;
Best Local Similarity 44.3%; Pred. No. 5.9e-22;
Matches 54; Conservative 22; Mismatches 43; Indels 3; Gaps 2;

```

```

QY 10 LALLQLAPAPVSPDAPGHR--KYVSWIDVYTRATCCPREVVVPLTVELMGTVAK 67
DB 12 LALLLYLHNAKSAQAPPTGEGKAEVKKFMDVYORSTCRPIETLVDFQETPEIETI 71
QY 68 LVPSCVTVORCGCCPRDGLCEVPTGOHVRMOILMIR-YPSOIGEMSLSEHSQCECRP 126
DB 72 FKPSCVPLMRGCGCCNDEALCEVPTSESNTTQIMRIKPHQSHIGEMSLFQHSRCECRP 131
QY 127 KK 128
DB 132 KK 133

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```

RESULT 4
Q96L82 PRELIMINARY: PRT: 191 AA.
AC Q96L82:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of vascular endothelial growth factor (VEGF) cDNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY047581; AAK95847.1; -.
SQ SEQUENCE 191 AA; 22314 MW; CCE57097DD3779BD CRC64;

```

```

Query Match 36.7%; Score 264; DB 4; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.9e-21;
Matches 54; Conservative 21; Mismatches 44; Indels 4; Gaps 2;

```

```

QY 10 LALLQLAPAPVSPDAPG---HQRKVSIDVYTRATCCPREVVVPLTVELMGTVAK 66
DB 12 LALLLYLHNAKSAQAPPAHEGGGQNHHEVKKFMDVYORSTCRPIETLVDFQETPEIETI 71
QY 67 QLVSCVTVORCGCCPRDGLCEVPTGOHVRMOILMIR-YPSOIGEMSLSEHSQCECR 125
DB 72 IFKPSCVPLMRGCGCCNDEALCEVPTSESNTTQIMRIKPHQSHIGEMSLFQHSRCECR 131
QY 126 PKK 128
DB 132 PKK 134

```

```

RESULT 5
Q96KJ0 PRELIMINARY: PRT: 191 AA.
AC Q96KJ0:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 165B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA Sugiono M., Winkler M., Gallatt D., Harper S.J., Bates D.O.;
RT "A new isoform of vascular endothelial growth factor mRNA is down-

```


Db 71 YIFKPSCVPLMRGAGCCNDESLCEVPTECYNTWQIMKIKPHISQIHMDMSFQOHSQCEC 130
 QY 125 RPKKK 129
 Db 131 RPKKE 135

RESULT 12

042572 ID 042572 PRELIMINARY; PRT; 194 AA.

AC 042572;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR 196.
 GN VEGF.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
 RT "Neovascularization of the Xenopus embryo."
 RL Dev. Dyn. 0:0-0(1997).
 DR EMBL; AF008594; AAB63680.1; -.
 DR HSSP; P15692; IYGH.
 DR InterPro; IPR000072; PDGF.
 DR Pfam; PF00341; PDGF_1.
 DR ProDom; PD001629; PDGF_1.
 DR SMART; SM00141; PDGF_1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 SQ SEQUENCE 194 AA; 22672 MW; 85D7BEC7CEFE17E CRC64;

Query Match 35.2%; Score 253; DB 13; Length 194;

Best Local Similarity 43.2%; Pred. No. 3.2e-20;
 Matches 54; Conservative 21; Mismatches 44; Indels 6; Gaps 3;

QY 10 LAALLQLAPQAQVPSOPDAPG---ORKKVSMIDVYTRATCOPREVVPLTVELMGTV 65
 Db 12 LAVLLYLPNQLSGAAR-MRGEQDHKPLEVYKFLKVIERSQVREILVDFQEPDEVE 70
 QY 66 KQLVPSCTVQRCGCCPDGLEGVPTGQHOVNRQIIMIR-YPSQSGEMSLSEHSQCEC 124
 Db 71 YIFKPSCVPLMRGAGCCNDESLCEVPTECYNTWQIMKIKPHISQIHMDMSFQOHSQCEC 130
 QY 125 RPKKK 129
 Db 131 RPKKE 135

RESULT 13

09BDE7 ID 09BDE7 PRELIMINARY; PRT; 126 AA.

AC 09BDE7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.

NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hazard T.M., Nayak N.R., Jia Y., Stouffer R.L.;
 RT "Rhesus macaque VEGF mRNA sequence."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

EMBL; AF339737; AAK26379.1; -.

DR HSSP; P15692; 2VPF.
 DR InterPro; IPR000072; PDGF.
 DR Pfam; PF00341; PDGF_1.
 DR ProDom; PD001629; PDGF_1.
 DR SMART; SM00141; PDGF_1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 FT NON_TER 1 1
 FT NON_TER 126 126
 SQ SEQUENCE 126 AA; 14599 MW; 1175F2386A83BCF CRC64;

Query Match 34.8%; Score 250; DB 6; Length 126;

Best Local Similarity 42.6%; Pred. No. 4.3e-20;
 Matches 52; Conservative 21; Mismatches 45; Indels 4; Gaps 2;

QY 10 LAALLQLAPQAQVPSOPDAPG---ORKKVSMIDVYTRATCOPREVVPLTVELMGTV 66
 Db 5 LALLLYLHNAKWSQAHNAHEGGQNNHNEVYKFMVYQSRYPLETVDFQEPDEIEY 64
 QY 67 QLVPSCTVQRCGCCPDGLEGVPTGQHOVNRQIIMIR-YPSQSGEMSLSEHSQCEC 125
 Db 65 IFKPSCVPLMRGAGCCNDESLCEVPTEESNTWQIMKIKPHISQIHMDMSFQOHSQCEC 124
 QY 126 PK 127
 Db 125 PK 126

RESULT 14

09MZB1 ID 09MZB1 PRELIMINARY; PRT; 118 AA.

AC 09MZB1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
 GN VEGF.

OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;

RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-PLACENTAL ARTERY ENDOTHELIUM;
 RC Zhang J., Tsol S.C., Magnus R.R.;
 RT "Growth factor expression in ovine fetal placental artery endothelial cells."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF250375; AAF75258.1; -.
 DR HSSP; P15692; IYVP.
 DR InterPro; IPR000072; PDGF.
 DR Pfam; PF00341; PDGF_1.
 DR ProDom; PD001629; PDGF_1.
 DR SMART; SM00141; PDGF_1.
 DR PROSITE; PS00249; PDGF_1; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 FT NON_TER 1 1
 FT NON_TER 118 118
 SQ SEQUENCE 118 AA; 13931 MW; 757DC53AA56378A6 CRC64;

Query Match 34.3%; Score 246.5; DB 6; Length 118;
 Best Local Similarity 45.2%; Pred. No. 9.7e-20;
 Matches 47; Conservative 21; Mismatches 33; Indels 3; Gaps 2;

QY 28 APQHQR--KVVSMIDVYTRATCOPREVVPLTVELMGTVARQVPSCTVQRCGCCPD 85
 Db 2 AEGGKPRHEVYKFMVYQSRYPLETVDFQEPDEIEYIFKPSCVPLMRGAGCCNDE 61
 QY 86 GLECVPTGQHOVNRQIIMIR-YPSQSGEMSLSEHSQCECRPK 128
 Db 62 SLECVPTGQHOVNRQIIMIR-YPSQSGEMSLSEHSQCECRPK 105

OX	NCBI_TaxID=8723;	
RN	[1]	
RP	SEQUENCE FROM N. A.	
RC	TISSUE=VENOM GLAND;	
RX	MEDLINE=21523945; PubMed=11517227;	
RA	Junqueira de Azevedo J. L. M., Farsky S. H. P., Oliveira M. L. S., Ho P. L.;	
RT	"Molecular Cloning and Expression of a Functional Snake Venom Vascular Endothelium Growth Factor (VEGF) from the Bothrops insularis Pit Viper. A New Member of the VEGF Family of Proteins."	
RT	J. Biol. Chem. 276:39836-39842(2001).	
DR	EMBL; AY033151; AAK52102.1; -.	
KW	Signal.	
FT	SIGNAL	
FT	1	24
FT	CHAIN	POTENTIAL.
FT	25	146
FT	SEQUENCE	VASCULAR ENDOTHELIAL GROWTH FACTOR.
FO	146 AA; 16356 MM; 066FC510D0CF46331 CR664;	

[illegible]

RESULT	19			
09N1S2				
ID	09N1S2	PRELIMINARY;	PRT;	78 AA.
AC	09N1S2:			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR ISOFORM 121 (FRAGMENT).			
GN	VEGF.			
OS	Capreolus capreolus (Roe deer).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;			
CC	Cervidae; Odocoileinae; Capreolus.			
OX	NCBI_TaxID=9858;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS;			
RA	MEDLINE=20532861; PubMed=11078967;			
RA	Wagener A., Blotner S., Gortiz F., Fickel J.;			
RT	"Detection of growth factors in the testis of roe deer (Capreolus			
RT	capreolus).";			
RL	Anim. Reprod. Sci. 64:65-75(2000).			
RL	EMBL; AF152593; AA073232.1; --.			
DR	HSSP; P15692; 2VPF.			
DR	InterPro; IPR000072; PDGF.			
DR	Pfam; PF00341; PDGF; 1.			
DR	ProDom; PD001629; PDGF; 1.			
DR	SMART; SM00141; PDGF; 1.			
DR	PROSITE; PS00249; PDGF_1; 1.			
DR	PROSITE; PS50278; PDGF_2; 1.			
FT	NON_TER	1		
FT	NON_TER	1		
SEQUENCE	78 AA: 9131 MW: 7520DDFFC17847C CRC64;			

Query Match	27.3%	Score 196.5	DB 6	Length 78;
Best Local Similarity	55.0%	Pred. No. 2	2e-14	
Matches	33;	Conservative	11;	Mismatches 15; Indels 1; Gaps 1
QY	70	PSCATVQRCGGCCPDGDECVPFGQHQVMMQIMLR	-YSSQLEGMSLEHHSOCCECPRK	128
		: : : : :		
Db	13	PSCVPLMRGCGCCNDESLCVTEEBENITMIMRKIPHGQIHGEMSFLOHNCCECPRK	72	
		: : : : :		

RESULT	20			
Q9N1S1				
ID	Q9N1S1	PRELIMINARY;	PRT;	123 AA.
AC	Q9N1S1;			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR ISOFORM 165 (FRAGMENT).			
VEBF.				
OS	Capreolus capreolus (Roe deer).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;			
CC	Cervidae; Odocolleinae; Capreolus.			
OX	NCBI_TaxID=9858;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS;			
RA	MEDLINE=20532861; PubMed=11078967;			
RA	Wagener A., Blotner S., Goritz F., Fickel J.;			
RT	"Detection of growth factors in the testis of roe deer (Capreolus			
RT	capreolus).";			
RL	Anim. Reprod. Sci. 64:65-75(2000).			
DR	EMBL; AF152594; AAF73233.1; --.			
DR	HSSP; P15692; IVGH.			
DR	InterPro; IPR000072; PDGF.			
DR	Pfam; PF00341; PDGF; 1.			
DR	ProDom; PD001629; PDGF; 1.			
DR	SMART; SM00141; PDGF; 1.			
DR	PROSITE; PS00249; PDGF_1; 1.			
DR	PROSITE; PS50278; PDGF_2; 1.			
FT	NON_TER	1		
FT	NON_TER	1		
SEQUENCE	123	123		
SEQUENCE	123 AA;	14354 MM;	0A756F54105A4CE1	CRC64;

	Query Match	27.3%	Score 196.5:	DB 6:	Length 123:
	Best Local Similarity	55.0%:	Pred. No. 3.5e-14:		
	Matches 33:	Conservative 11:	Mismatches 13:	Indels 1:	Gaps 1:
Oy	70	PSCVTATGAGCGCCPDGECVPTGGHQVMQIMLTR-YPSOLSGEMSLSEHSQCCECPKPK	128		
		: : :			
Dd	13	PSCVLMRGCGCNDSELCVTEEFENITMQIRLPHFGHGIGIESSFLQHNKCCECRPK	72		
		: : :			

RESULT	21			
018843				
1D	018843	PRELIMINARY;	PRT;	75 AA.
AC	018843;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).			
GN	VEGF.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI TAXID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NEW ZEALAND WHITE; TISSUE=SKELETAL MUSCLE;			
RA	MEDLINE=96191144; PubMed=9530113;			
RA	Skeirjanc D., Jaschinski F., Heine G., Pette D.;			
RT	"Sequential increases in capillarization and mitochondrial enzymes in			
RT	low-frequency-stimulated rabbit muscle.";			
RL	Am. J. Physiol. 274:C810-C818(1998).			
DR	EMBL; AF022179; AAC15469.1; -.			
DR	HSSB; P15692; 2VPF.			
DR	InterPro; IPR000072; PDGF.			
DR	Pfam; PF00341; PDGF_1.			
DR	ProDom; PD001629; PDGF_1.			
DR	SMART; SM00141; PDGF_1.			
DR	PROSITE; PS00249; PDGF_1; 1.			

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DR PROSITE; PSS0278; PDGF_2; 1.
FT NON_TER 1
RP NON_TER 75
SQ SEQUENCE 75 AA; 8720 MW; DDE2C5B29E69359 CRC64;

Query Match
Best Local Similarity 26.5%; Score 190.5; DB 6; Length 75;
Matches 33; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 76 PSCVTVOGCGCCPDGLEGVPTGQHVYRMQIMIR-YFSSQIGEMSLSEHSQCECRP 127
Db 17 PSCVPIVRGCGCCNDSLECVPTGEFVYTMQIMIRKPHQGHIGEMSLQHNKCECRP 75

RESULT 22
Q9YMF3 PRELIMINARY; PRT; 132 AA.
AC 09YMF3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOIOG VEGF-E.
OS Orf virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OX NCBI_Taxid=10258;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D1701;
RX MEDLINE=99107753; PubMed=9889193;
RA Meyer M., Claus M., Lepple-Wienhues A., Waltenberger J.,
RA Augustin H.G., Ziche M., Ianz C., Buettner M., Rziha H.J., Dehio C.;
RT "A novel vascular endothelial growth factor encoded by orf virus.
RT VEGF-E, mediates angiogenesis via signalling through VEGFR-2 (KDR) but
RT not VEGFR-1 (Flt-1) receptor tyrosine kinases."
RL EMBO J. 18:363-374(1999).
DR EMBL; AF106020; AAD03735.1; -.
DR HSSP; P15692; 1VP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 132 AA; 14763 MW; 15F403A06B872926 CRC64;

Query Match
Best Local Similarity 25.9%; Score 186.5; DB 12; Length 132;
Matches 33; Conservative 20; Mismatches 37; Indels 1; Gaps 1;

QY 37 SMIDVYTRATCCPREVYVLTVMGTAKQLVPSCVTVQRCGCCPDGLEGVPTGQIMQ 96
Db 25 TISEVFENGCKRPFRVENVHDEHPELTQRENPCCVTILMRGCGCCNDSLECVPTGEAN 84

QY 97 VEMQILMIRYPSQ-LGEMSLSEHSQCECRP 126
Db 85 VTMQLMGASVSGNGMQLHSLFVEHKKCDCKP 115

RESULT 23
Q70123 PRELIMINARY; PRT; 141 AA.
AC 070123;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE VEGF115.
GN VEGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=95101726; PubMed=7803491;
RA Sugihara T., Kaul S.C., Mitsui Y., Wadhwa R.;
RT "Enhanced expression of multiple forms of VEGF is associated with
RT spontaneous immortalization of murine fibroblasts."
RL Biochim. Biophys. Acta 1224:365-370(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=98112857; PubMed=9446618;
RA Sugihara T., Wadhwa R., Kaul S.C., Mitsui Y.;
RT "A novel alternatively spliced form of murine vascular endothelial
RT growth factor, VEGF 115."
RL J. Biol. Chem. 273:3033-3038(1998).
DR EMBL; U50279; AAC05442.1; -.
DR HSSP; P15692; 1VP.
DR MGD; MGI:103178; Vegf.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 141 AA; 15550 MW; A27C4EF5A7071338 CRC64;

Query Match
Best Local Similarity 25.7%; Score 185; DB 11; Length 141;
Matches 37; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

QY 10 LAILDLAPAAQVNSQPDAPGHOR--KYVSMIDVYTRATCCPREVYVLTVMGTAKQ 67
Db 12 LAILTLHRAKKSQAAPTTBEGQKSHVTKEMDVYRSTCRPLETVDTITQETPDEIYI 71

QY 68 LVPSCVTVOGCGCCPDGLEGVPTGQHVYRMQI 101
Db 72 FRPSCVPIVRGCGCCNDSLECVPTGESNTIMQV 105

RESULT 24
Q088911 PRELIMINARY; PRT; 110 AA.
AC 088911;
AD 088911;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR A 110 (FRAGMENT).
GN VEGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=PENIS;
RX MEDLINE=99115228; PubMed=9916007;
RA Burchard M., Burchard T., Chen M.W., Shabsigh A., de la Taille A.,
RA Burtan R., Shabsigh R.;
RT "Expression of messenger ribonucleic acid splice variants for vascular
RT endothelial growth factor in the penis of adult rats and humans."
RL Biol. Reptod. 60:398-404(1999).
DR EMBL; AF080594; AAC36708.1; -.
DR HSSP; P15692; 1VP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1

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SQ SEQUENCE 110 AA: 12713 MW: B81B79AC08D89F06 CRC64:

Query Match 25.6%; Score 184; DB 11; Length 110;
Best Local Similarity 34.2%; Pred. No. 7.6e-13;
Matches 39; Conservative 15; Mismatches 38; Indels 22; Gaps 2;

OY 21 APVSOPDAGHQRKVSMDVYTRATCOPREVYPLTVELMGVAQOLVPSCTVQRCGG 80
DB 1 APTBEGQRAHE--VVKEMDVYQRSYCRPIETLVDFIQEYPRDEIYFKRSCVPLMRACAG 58

OY 81 CDPDDLECVPTGOHVRMOILMIRYPSOLGEMSLSEHSOCRCPRKKDSAYK 134
DB 59 CCNDELAEVPTSESNVTMO-----TCCKSCKNDSRCK 92

RESULT 25

OY1ZE4 PRELIMINARY: PRT: 326 AA.

AC OY1ZE4:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE VEGF-D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Kiriln V., Maritschek R., Krishnan J., Steffen A., Waltenberger J.,
RA Pepper M.S., Giansis A., Sleeman J.P.;
RT "Characterization of indolinones which specifically inhibit VEGF-C and
RT VEGF-D-induced activation of VEGFR-3 but not VEGFR-2.";
RL Eur. J. Biochem. 0:0-0(2001).
DR EMBL; AY032728; AAK96008.1; -
SQ SEQUENCE 326 AA: 37106 MW: D7CAEBA6C9FABR7D CRC64:

Query Match 20.8%; Score 149.5; DB 11; Length 326;
Best Local Similarity 32.3%; Pred. No. 1.6e-08;
Matches 31; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

OY 34 KYVSMIDVYTRATCOPREVYPLTVELMGVAQOLVPSCTVQRCGGCCDDGLECVPTG 93
DB 105 KYID--EEMQRTQCPRECEVASELIGTNTTFKPCVNVPRCGGCCNEESVMCMNTS 162

OY 94 OHQVRMOILMIRYPSOLGEM--SLSEHSOCRCRP 126
DB 163 TSYISKQLEFISVPLTSVPELVVVKIANHTGCKCLP 198

RESULT 26

OY7500 PRELIMINARY: PRT: 68 AA.

AC OY7500:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE VASCUAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
GN VEGF.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Inoue K., Kawabe Y., Kodama T.;
RT "Rabbit VEGF cDNA, partial."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020216; BAA36949.1; -
HSSP; P15692; 2VPE.

DR InterPro: IPR000072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
FT NON_TER 1 68
SQ SEQUENCE 68 AA: 7819 MW: 687638661E98DEE0 CRC64:

Query Match 20.7%; Score 149; DB 6; Length 68;
Best Local Similarity 47.5%; Pred. No. 3.4e-09;
Matches 28; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

OY 47 COPREVYPLTVELMGVAQOLVPSCTVQRCGGCCDDGLECVPTGOHVRMOILMIR 105
DB 6 COPLETVDFIQEYPRDEIYFKRSCVPLVRCGCCNDELAEVPTSESNVTMOIMRIK 64

RESULT 27

OY7352 PRELIMINARY: PRT: 418 AA.

AC OY7352:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE VASCUAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN VEGF-C.
OS Coturnix coturnix (common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98167900; PubMed=9435294;
RA Eichmann A., Corbel C., Jaffredo T., Breant V., Joukov V., Kumar V.,
RA Altalo K., Le Douarin N.M.;
RT "Avian VEGF-C: cloning, embryonic expression pattern and stimulation
RT of the differentiation of VEGFR2 expressing endothelial cell
RT precursors.";
RL Development 125:743-752(1998).
DR EMBL; Y15837; CAA75799.1; -
DR HSSP; P15692; 1VPE.

DR InterPro: IPR004153; CXKC.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF03128; CXKC; 6.
DR Pfam: PF00341; PDGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00067; GHA; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
KW signal.
FT CHAIN 1 31
SQ SEQUENCE 418 AA: 46839 MW: 099BFC79151BF2B CRC64:

Query Match 20.7%; Score 149; DB 13; Length 418;
Best Local Similarity 31.7%; Pred. No. 2.4e-08;
Matches 33; Conservative 16; Mismatches 51; Indels 4; Gaps 2;

OY 28 APBHQKRVSMIDVYTRAT--COPREVYPLTVELMGVAQOLVPSCTVQRCGGCCDDG 86
DB 110 AAHYNAELIKSIDTEWKKTCMPRECVVDGKEGATNTFFKPCVSIYRCGCCNSEG 169

OY 87 LECVPTGOHVRMOILMIRYPSOLGEM--MSLEHSOCRCRPK 127
DB 1 LECVPTGOHVRMOILMIRYPSOLGEM--MSLEHSOCRCRPK 127

Db 170 LQCMNTSTGYLSKTLFEITVPLSGPKPVTYSFANHNSCRMSK 213

RESULT 28

0912H6 PRELIMINARY; PRT; 326 AA.

AC 0912H6; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR C (FRAGMENT).

OS Meiones unguiculatus (Mongolian jird).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.

NCBI_TaxID=10047;

OX NCBI_TaxID=10047;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LONG;

RA Panlailais B.J., Fuhrman J.A.;

RT "Brugia malayi stimulates VEGF-C, a growth factor specific for lymphatic endothelium, by an indirect mechanism."

RT Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF32867; AAL28127.1; -.

FT NON_TER 1

SQ SEQUENCE 326 AA; 36826 MW; DOB2772C77836914 CRC64;

Query Match 20.4%; Score 147; DB 11; Length 326;

Best Local Similarity 32.7%; Pred. No. 3,1e-08;

Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

Db 18 AAHYTETLKSIDNEMRKTCQMPREVCIDVGKEFGAATNTFFKPCVSVYRCGCCNSEG 77

QY 87 LECVPTGQHVMOQIMIRYSSQIGF--MSLEHSCQECRPR 127

DB 78 LQCMNTSTGYLSKTLFEITVPLSGPKPVTYSFANHNSCRMSK 121

RESULT 29

0912E3 PRELIMINARY; PRT; 415 AA.

AC 0912E3; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE VEGF-C.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY;

RA Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,

RA Pepper M.S., Giannis A., Sleeman J.P.;

RT "Characterization of indolinones which specifically inhibit VEGF-C and VEGF-D-induced activation of VEGFR-3 but not VEGFR-2."

RT EMBL; AY032729; AAK96009.1; -.

DR SEQUENCE 415 AA; 46397 MW; 1EB677F5B260A525 CRC64;

Query Match 20.4%; Score 147; DB 11; Length 415;

Best Local Similarity 32.7%; Pred. No. 4e-08;

Matches 34; Conservative 15; Mismatches 51; Indels 4; Gaps 2;

Db 107 AAHYTETLKSIDNEMRKTCQMPREVCIDVGKEFGAATNTFFKPCVSVYRCGCCNSEG 166

QY 87 LECVPTGQHVMOQIMIRYSSQIGF--MSLEHSCQECRPR 127

DB 167 LQCMNTSTGYLSKTLFEITVPLSGPKPVTISFANHNSCRMSK 210

RESULT 30

09XS50 PRELIMINARY; PRT; 420 AA.

AC 09XS50; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART;

RA MEDLINE=20044783; PubMed=10575000;

RA Yonekura H., Sakurai S., Liu X., Migita H., Wang H., Yamagishi S.,

RA Nomura M., Abedin M.J., Uno K. H., Yamamoto Y., Yamamoto H.;

RT "Placenta growth factor and vascular endothelial growth factor B and C expression in microvascular endothelial cells and pericytes."

RT Implication in autocrine and paracrine regulation of angiogenesis.";

RT J. Biol. Chem. 274:35172-35178(1999).

DR EMBL; AB004275; BAA7687.1; -.

DR HSSP; P15692; IVP.

DR InterPro; IPR004153; CXXC.

DR InterPro; IPR000072; PDGF.

DR Pfam; PF00341; PDGF_1.

DR Pfam; PF001629; PDGF_1.

DR SMART; SM00141; PDGF_1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS50278; PDGF_2; 1.

KW SIGNAL.

FT SIGNAL 1 20 POTENTIAL.

FT CHARIN 21 420 VASCULAR ENDOTHELIAL GROWTH FACTOR C.

SQ SEQUENCE 420 AA; 46681 MW; 58BA8431A3C8E2D CRC64;

Query Match 19.6%; Score 141; DB 6; Length 420;

Best Local Similarity 31.7%; Pred. No. 1,9e-07;

Matches 33; Conservative 15; Mismatches 52; Indels 4; Gaps 2;

QY 28 APGHQKRVSMIDYTRAT-COPREVVPPLVVELMGTVAKQLVPSCTVYORCGCCPDDG 86

DB 112 AAHYTETLKSIDNEMRKTCQMPREVCIDVGKEFGAATNTFFKPCVSVYRCGCCNSEG 171

QY 87 LECVPTGQHVMOQIMIRYSSQIGF--MSLEHSCQECRPR 127

DB 172 QQCMNTSTGYLSKTLFEITVPLSGPKPVTISFANHNSCRMSK 215

RESULT 31

09BLX1 PRELIMINARY; PRT; 314 AA.

AC 09BLX1; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE PDGF/VEGF FACTOR-1 PRECURSOR.

GN PVF1.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RN [1]

```
RP SEQUENCE FROM N.A.
RA Helio T.I., Wahlstroem G., Kaerpenen T., Pulkkinen M., Alltalo K.,
RA Roos C.;
RT "Drosophila PDGF/VEGF receptor homolog is specifically expressed in
RT hemocytes.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ401391; CAC24699.1; -
DR InterPro: IPR004153; CXKCXC.
DR InterPro: IPR00072; PDGF.
DR Pfam: PF03128; CXKC; 3.
DR Pfam: PF00341; PDGF; 1.
DR PRODOM: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 314 PDGF/VEGF FACTOR-1.
SQ SEQUENCE 314 AA; 34482 MW; DE7771E7B2BD5EDD CRC64;

Query Match 19.2%; Score 138; DB 5; Length 314;
Best Local Similarity 26.9%; Pred. No. 2.9e-07;
Matches 39; Conservative 29; Mismatches 61; Indels 16; Gaps 5;

QY 2 SPLRLRLALLQLAPQAPVS--QPDAPGHQKRV--SWIDVYTRATCOPREVVPLT 57
DB 82 TPRLPLPLSVSELTNTVADYVSGEMPSSEKFNKSIKTVRNATPASCSPQPIVELK 141
QY 58 VELMGTVAKOLVPSCVTVQVQGGCCPDGELCEVPTGQHVQMIIMI-----RYPSSQ 110
DB 142 PPAEDENAYYYWPACTRISSRCNGCCGSLISQCPTEVQVQLRVKVKVRAATSGRRPTI 201
QY 111 LGEMSLERHSQ--CECRPKKDSAY 133
DB 202 I---TVEQHTQCRDCRCKRAEDCNV 223

RESULT 32
QY 096028 PRELIMINARY; PRT; 325 AA.
AC 096028;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LD28763P.
GN CG7103.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Abpayani A., Carlson J.,
RA Champé M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Paclé J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY051751; AAK93175.1; -
SQ SEQUENCE 325 AA; 35779 MW; D215BC47DCAAFDPD CRC64;

Query Match 19.2%; Score 138; DB 5; Length 325;
Best Local Similarity 26.9%; Pred. No. 3e-07;
Matches 39; Conservative 29; Mismatches 61; Indels 16; Gaps 5;

QY 2 SPLRLRLALLQLAPQAPVS--QPDAPGHQKRV--SWIDVYTRATCOPREVVPLT 57
DB 93 TPRLPLPLSVSELTNTVADYVSGEMPSSEKFNKSIKTVRNATPASCSPQPIVELK 152
QY 58 VELMGTVAKOLVPSCVTVQVQGGCCPDGELCEVPTGQHVQMIIMI-----RYPSSQ 110
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DB 153 PPAEDENAYYYWPACTRISSRCNGCCGSLISQCPTEVQVQLRVKVKVRAATSGRRPTI 212
QY 111 LGEMSLERHSQ--CECRPKKDSAY 133
DB 213 I---TVEQHTQCRDCRCKRAEDCNV 234

RESULT 33
QY 09VWP6 PRELIMINARY; PRT; 301 AA.
AC 09VWP6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CG7103.
GN CG7103.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champé M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abtil J.F., Abdayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jafar M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jialali M., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclé J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
DR EMBL: AE003510; AAF4892.2; -
DR FLYBase: FBgn0030964; Pvfl.
DR InterPro: IPR00072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR PRODOM: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 301 AA; 33013 MW; 4C45D988AAC9A5A9 CRC64;
```

Query Match	18.78;	Score 134.5;	DB 5;	Length 301;
Best Local Similarity	26.08;	Pred. No. 6.9e-07;		
Matches 38;	Conservative 30;	Mismatches 61;	Indels 17;	Gaps 5

QY 2 SPLRLRLIALLIQLAPRQAPVS--QPDAREHQKRV--SWIDYTRATCQPREVVPL 566
:|| |::|| | | : : : : : | | : | |
Db 93 TPLTLPISVSAELTNVTADYDVSGEMPSSKNEFKRSIMKSAITRNATPASCSPQITVEL 15

```

QY 57 TVELMGTVARQLVPSCVTYVQRRGGCCPPDGLCEPTGHOHYRMQIMI-----RIPSS 109
      ::::: ||||| : ||| ||::: : |||
Db 153 KPPAEDEANYYMPACTRISRCNGCCGSLISCPTEVEGEVQLRVRRKVDRAATSGRRPET 212

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Oy 110 QLGEMSLFEHSQ--CECRPKKKDSAV 133
Db 213 I I--TVEQHTQCRCDCRTKAEDCNV 235

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RESULT	34
QCUC96	
ID	QCUC96
AC	QCUC96;
DT	01-JUN-2001 (Tremblrel, 17, Created)
DT	01-JUN-2001 (Tremblrel, 17, last sequence update)
DT	01-DEC-2001 (Tremblrel, 19, last annotation update)
DE	11 DAYS PREGNANT ADULT FEMALE OVARY AND UTERUS CDNN, RIKEN FULL-LENGTH
DE	ENRICHED LIBRARY, CLONE:5033413018, FULL INSERT SEQUENCE
DE	(FRAGMENT)

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=OVARY, AND UTERUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamamaka I.,
RA Salto T., Okazaki Y., Gotojiori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carncini P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hornum W., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y..
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RZ EMBL; AK017169; BAB30622.1; -.
DR HSSP; P01127; IPDG.
DR MGD; MGI:97527; PdGfa.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF_1.
DR ProDom; PD001629; PDGF_1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1.
DR PROSITE; PS50278; PDGF_2.
FT NON_CODING
SQ
SEQUENCE 118 AA; 13551 MW; 00B51AB7C6E050D6 CRC64;

Query Match	17.7%;	Score 127;	DB 11;	Length 118;
Best Local Similarity	31.3%;	Pred. No. 1.7e-06;		
Matches	31;	Conservative	20;	Mismatches 36;
			Indels	12;
			Gaps	5

Qy 45 ATCQREVV---VPLTLEMLGNVALOL--PSCVYTORQGGCGGCRDGLCEVRYGNDQVMOI 109
Db 16 AVCKRRIYIYELPRNS-QVDPRISANFLIIPRCEVLEVKRKGCGGCSNTSVAKQSRVRYHNRSVKV 74
Qy 102 LMIRY----PSSQLGEMSLSEHSQCECPKKKSDAVUPD 136
Db 75 AKVEYVKKRPRIKEOVYVLEHLEDCAC---ATSNLMD 109

RESULT	35	
Q99L56		
ID	Q99L56	PRELIMINARY;
		PRT;
		196 AA.

DN 01-JUN-2001 (TREMBLER, 17, last sequence update)
 DT 01-DEC-2001 (TREMBLER, 19, last annotation update)
 DE PLATELET DERIVED GROWTH FACTOR, ALPHA.
 PGFA.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

KA Stralsberg K.;
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003817; AAH03817.1; -.
 DR HSSP: P01127; 1PBG.
 DR MGD; MGI:97527; pdgfa.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF. 1.
 DR ProDom: PD001629; PDGF. 1.
 DR SMART: SM00141; PDGF. 1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 DR SSOURCE 196 AA; 22280 MW; 2610178BPACCA3647 CRC64;

	Query Match	17.7%	Score 127;	DB 11;	Length 196;
	Best Local Similarity	31.3%;	Pred. No. 2.9e-06;		
	Matches 31; Conservative	20;	Mismatches 36;	Indels 12;	Gaps 5.
QY	45 ATCCGREVV--VPLVLGLMGTVAKQLV-PSCVTYORCGGGCCPDDLGLECVPTGQHVRMOI	101			
	: : : : : : : : : : : : : : : :				
DQ	94 AVCKRTVIYLPRIS-QVDPTSANFLIMPPCEYKRCGTGCCTSSVKCOPSRVHNHRSVKV	152			
QY	102 LMIRY----PSSQLGEMSLSEHSOCECRPKKKDSAVKPD	136			
	: : : : : : : : : : : : : : : :				
DQ	153 AKVEYRKRPKLKEQVRLREHLDECAC---ATSNLNDP	187			

RESULT	36
Q29613	
ID	Q29613
PRELIMINARY:	
PRT:	210 AA.

DT 01-NOV-1996 (TREMBL). 01, Created)
 DT 01-NOV-1996 (TREMBL). 01, last sequence update)
 DT 01-JUN-2001 (TREMBL). 17, last annotation update)
 DE C-SIS ONCOGENE (PLATELET-DERIVED GROWTH FACTOR).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxId=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=871446463; PubMed=3822831;
 RX van den Ouweland A.M.W., van Grooten J.J.M., Schaalken J.A.,
 RY van Neck H.W., Bloemers P.J., Van de Ven W.J.M.,
 RT "Genetic organization of the c-Sis transcription unit.",
 RL Nucleic Acids Res. 15:959-970(1987).
 RN [2]
 RP SEQUENCE OF 1-21 FROM N.A.

```

Best Local Similarity 28.8%; Pred. No. 5.3e-06;
Matches 34; Conservative 20; Mismatches 36; Indels 28; Gaps 6;

Oy 45 ATCCGEEVY--VPLVYELMGTVAKOLY-PSCTYVRCGCGCCPDGGLCEVPTGQHOVMOI 101
Db 94 AACKRTVYIYELPR-SQDPTSPANLIMPVEVAKRCCTGCTSSVKCPISRHHRSVAV 152

Oy 102 LMIRY-----PSSQLGEMSLSEHSQCEC-----RP-----KKKDSAVKP 135
Db 153 AKVEYVRKKPKLKEVLVRLEEHECTCTSTNNSDIREEETGRPRESGKKRRKKIKP 210

RESULT 38
O90W23
ID O90W23 PRELIMINARY: PRT: 251 AA.
AC O90W23;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR B CHAIN PRECURSOR,
GN PDGF-B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGRON;
```

RT	factor-B chain cDNA."	EMBL/GenBank/DBJ databases.
RL	Submitted (Aug-1999)	to the
DR	EMBL; AB031025; BAB64307.1;	"
KM	Signal.	
FT	SIGNAL	1 31
FT	CHAIN	88 196
SO	SEQUENCE	251 AA; 28515 MW; 52B096C938C4298A CRC64;
Query Match	17.4%;	Score 125; DB 13; Length 251;
Best Local Similarity	30.0%;	Pred. No. 6; 4e-06;

QY	45	ANCQREVVVPLITVELMGVAKOLV--PSCVAYVRGCGCCPDDELCVTPTGOHVNMJLL	102
	:	: : : :	: : : :
Dd	102	ACEKTRTVFELISRDWVDSTNANFWVPMPCEVQRCSGCCNNRNMQCRPM---	QIRVRHY 158
QY	103	MT-----RYPSSQLGEMSLSEHSQEC---RPKKKS	131
	:	: : : : :	: :
Dd	159	QVNKTIEFFQRKPFIKFVKIVPLEDHVQCREEVVSRRPPRSN	198
RESULT	39		
ID	Q15354	PRELIMINARY;	PRT; 185 AA.
AC	Q15354		
Dt	01-NOV-1996	(TREMBLrel. 01, Created)	
Dt	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
Dt	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	ORF 2	PROTEIN (FRAGMENT).	
CN	GN	ORF 2.	
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
NCBI_TaxID=9606;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=CHORIOCARCINOMA;		
RC	MEDLINE=9538493; PubMed=7659502;		
RA	Dicks R.P.H., Onnekink C., Jansen H.J., de Jong A., Bloemers H.P.J.;		
RT	"A novel human C-sis mRNA species is transcribed from a promoter in c-		
RT	sis intron 1 and contains the code for an alternative PDGF B-like		


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DB 94 AVCKTRVYIETPRS-QIDPISANFLIWPCEVYKRCCTGCGCNTSVKCPSPRIHHSVKY 152
QY 102 LMIRY-----PSSOLGEMSLSEHSQCCECRPKKDS 131
DB 153 AKVEYVKKRPKLEKVLVRLSEHMECTCTSTINTNS 186

RESULT 43
Q9WV07 PRELIMINARY; PRT; 149 AA.
AC Q9WV07;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PDGF A (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AB028637; BAA78768.1; -.
DR HSSP; P01127; IPDG.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1 149
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16963 MW; C93814FA6D041A65 CRC64;

Query Match 16.8%; Score 121; DB 11; Length 149;
Best Local Similarity 31.3%; Pred. No. 1e-05;
Matches 31; Conservative 18; Mismatches 38; Indels 12; Gaps 5;

QY 45 ATGCPREVV--VPLTVELMGTAKOLY-PSCYTVYORCGCCPDGGLCEVPTGQHQVMOI 101
DB 53 AVCKTRVYIETPRS-QADPTSANFLIWPCEVYKRCCTGCGCNTSVKCPSPRIHHSVKY 111
QY 102 LMIRY-----PSSOLGEMSLSEHSQCCECRPKKDSAVKPD 136
DB 112 AKVEYVKKRPKLEKVLVRLSEHMECTCTSTINTNS 146

RESULT 44
Q9PUF7 PRELIMINARY; PRT; 211 AA.
AC Q9PUF7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR A-CHAIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20302546; PubMed=10842055;
RA Ataliois P.;
RT "Platelet-derived growth factor A modulates limb chondrogenesis both
in vivo and in vitro."
Mech. Dev. 94:13-24(2000).
EMBL: AF188841; AAF01459.1; -.
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DR HSSP; P01127; IPDG.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 211 AA; 24349 MW; 1A6AA3A5DBD42382 CRC64;

Query Match 16.7%; Score 120; DB 13; Length 211;
Best Local Similarity 30.9%; Pred. No. 1.9e-05;
Matches 29; Conservative 18; Mismatches 39; Indels 8; Gaps 4;

QY 45 ATGCPREVV--VPLTVELMGTAKOLY-PSCYTVYORCGCCPDGGLCEVPTGQHQVMOI 101
DB 94 AVCKTRVYIETPRS-QIDPISANFLIWPCEVYKRCCTGCGCNTSVKCPSPRIHHSVKY 152
QY 102 LMIRY-----PSSOLGEMSLSEHSQCCECRPKKDS 131
DB 153 AKVEYVKKRPKLEKVLVRLSEHMECTCTSTINTNS 186

RESULT 45
Q9DE50 PRELIMINARY; PRT; 195 AA.
AC Q9DE50;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR A CHAIN.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu L.; Balasubramanian N.V.; Ge R.;
RT "The zebrafish PDGF-A/PDGF-R-alpha signalling system in early
embryogenesis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF200950; AAG43478.1; -.
DR HSSP; P01127; IPDG.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 195 AA; 22618 MW; 49B25831E1975604 CRC64;

Query Match 16.0%; Score 115; DB 13; Length 195;
Best Local Similarity 29.4%; Pred. No. 6.2e-05;
Matches 30; Conservative 22; Mismatches 40; Indels 10; Gaps 6;

QY 31 HOKRVSNIDVYTRATQCPREVV--VPLTVELMGTAKOLY-PSCYTVYORCGCCPDG 86
DB 80 HSRKRS-IEAVPAVCKTRVYIETPRS-QVDTANFLIWPCEVYKRCCTGCGCNTSVK 137
QY 87 LECVPTGQHQVMOILMIRY-----PSSOLGEMSLSEHSQCCEC 124
DB 138 MRCHPSKKHHRNVAVKVEYVRRRPKLEKVLVRLSEHMECTCTSTINTNS 179
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Search completed: September 10, 2002, 02:59:06
Job time: 539 sec

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